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PROVISIONAL APPLICATION FOR PATENT COVER SHEET

This is a request for filing a PROVISIONAL APPLICATION FOR PATENT under 37 CFR 1.53(c).

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METHODS FOR IDENTIFYING RISK OF OSTEOARTHRITIS AND TREATMENTS THEREOF					
Direct all correspondence to: CORRESPONDENCE ADDRESS					
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[Page 1 of 2]

Respectfully submitted,

Date April 1, 2004

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**METHODS FOR IDENTIFYING RISK OF OSTEOARTHRITIS AND
TREATMENTS THEREOF**

Field of the Invention

[0001] The invention relates to genetic methods for identifying risk of osteoarthritis and treatments that specifically target such diseases.

Background

[0002] Osteoarthritis (OA) is a chronic disease usually affecting weight-bearing synovial joints. There are approximately 20 million Americans affected by OA and it is the leading cause of disability in the United States. In addition to extensive human suffering, OA also accounts for nearly all knee replacements and more than half of all hip replacements in the United States. Despite its prevalence, OA is poorly understood and there are few treatments available besides anti-inflammatory drugs and joint replacement.

[0003] Most commonly affecting middle-aged and older people, OA can range from very mild to very severe. It affects hands and weight-bearing joints such as knees, hips, feet and the back. Knee OA can be as disabling as any cardiovascular disease except stroke.

[0004] OA is characterized by the breakdown of cartilage in joints. Cartilage in joints cushions the ends of bones, and cartilage breakdown causes bones to rub against each other, causing pain and loss of movement. Type II collagen is the main component of cartilage, comprising 15-25% of the wet weight, approximately half the dry weight, and representing 90-95% of the total collagen content in the tissue. It forms fibrils that endow cartilage with tensile strength (Mayne, R. Arthritis Rheum. 32:241-246 (1989)).

Summary

[0005] It has been discovered that certain polymorphic variations in human genomic DNA are associated with osteoarthritis. In particular, polymorphic variants in loci containing *KIAA0296*, *chrom 4* and *SNW1* regions and other regions in Table A of human genomic DNA have been associated with risk of osteoarthritis.

[0006] Thus, featured herein are methods for identifying a subject at risk of osteoarthritis and/or a risk of osteoarthritis in a subject, which comprise detecting the presence or absence of one or more polymorphic variations associated with osteoarthritis in or around the loci described herein in a human nucleic acid sample. In an embodiment, two or more polymorphic variations are detected in two or more regions of which one is the *KIAA0296*, *chrom 4* or *SNW1* region or other region in Table A. In certain

embodiments, 3 or more, or 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 or more polymorphic variants are detected.

[0007] Also featured are nucleic acids that include one or more polymorphic variations associated with occurrence of osteoarthritis, as well as polypeptides encoded by these nucleic acids. In addition, provided are methods for identifying candidate therapeutic molecules for treating osteoarthritis, as well as methods for treating osteoarthritis in a subject by identifying a subject at risk of osteoarthritis and treating the subject with a suitable prophylactic, treatment or therapeutic molecule.

[0008] Also provided are compositions comprising a cell from a subject having osteoarthritis or at risk of osteoarthritis and/or a *KIAA0296*, *chrom 4* or *SNW1* nucleic acid or other nucleic acid referenced in Table A, with a RNAi, siRNA, antisense DNA or RNA, or ribozyme nucleic acid designed from a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A. In an embodiment, the RNAi, siRNA, antisense DNA or RNA, or ribozyme nucleic acid is designed from a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A that includes one or more polymorphic variations associated with osteoarthritis, and in some instances, specifically interacts with such a nucleotide sequence. Further, provided are arrays of nucleic acids bound to a solid surface, in which one or more nucleic acid molecules of the array have a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A, or a fragment or substantially identical nucleic acid thereof, or a complementary nucleic acid of the foregoing. Featured also are compositions comprising a cell from a subject having osteoarthritis or at risk of osteoarthritis and/or a *KIAA0296*, *chrom 4* or *SNW1* polypeptide or other polypeptide referenced in Table A, with an antibody that specifically binds to the polypeptide. In an embodiment, the antibody specifically binds to an epitope in the polypeptide that includes a non-synonymous amino acid modification associated with osteoarthritis (e.g., results in an amino acid substitution in the encoded polypeptide associated with osteoarthritis). In certain embodiments, the antibody selectively binds to an epitope in the *KIAA0296*, *chrom 4* or *SNW1* polypeptide, or other polypeptide referenced in Table A, having an amino acid associated with osteoarthritis. Thus, featured is an antibody that binds an epitope having an amino acid encoded by rs734784, rs1042164, rs749670, rs955592 and/or rs1040461, such as a valine or isoleucine encoded by rs734784 (e.g., a valine at position 489 in a *KCNS1* polypeptide), a valine or alanine encoded by rs1042164 (e.g., a valine at position 133 in a *ETRI01* polypeptide), a glutamate or glycine encoded by rs749670 (e.g., a glutamate at position 327 in a *KIAA0296* polypeptide), a threonine or isoleucine encoded by rs955592 (e.g., a threonine at position 70 in a *FLJ21977* polypeptide) or a glycine or serine encoded by rs1040461 (e.g., a glycine at position 207 in a *RAB23* polypeptide) at the corresponding position in the polypeptide.

Brief Description of the Drawings

[0009] Figures 1A-1C show proximal SNPs in *KIAA0296*, *chrom 4* and *SNW1* regions of genomic DNA, respectively. The position of each SNP in the chromosome is shown on the x-axis and the y-axis provides the negative logarithm of the p-value comparing the estimated allele to that of the control group. Also shown in the figures are exons and introns of the regions in the approximate chromosomal positions.

Detailed Description

[0010] It has been discovered that a polymorphic variant in a locus containing a *KIAA0296*, *chrom 4* or *SNW1* region is associated with occurrence of osteoarthritis in subjects. Thus, detecting genetic determinants associated with an increased risk of osteoarthritis occurrence can lead to early identification of a predisposition to osteoarthritis and early prescription of preventative measures. Also, associating a *KIAA0296*, *chrom 4* or *SNW1* polymorphic variant and other variants referenced in Table A with osteoarthritis has provided new targets for screening molecules useful in treatments of osteoarthritis.

Osteoarthritis and Sample Selection

[0011] Osteoarthritis (OA), or degenerative joint disease, is one of the oldest and most common types of arthritis. It is characterized by the breakdown of the joint's cartilage. Cartilage is the part of the joint that cushions the ends of bones, and its breakdown causes bones to rub against each other, causing pain and loss of movement. Type II collagen is the main component of cartilage, comprising 15-25% of the wet weight, approximately half the dry weight, and representing 90-95% of the total collagen content in the tissue. It forms fibrils that endow cartilage with tensile strength (Mayne, R. Arthritis Rheum. 32:241-246 (1989)).

[0012] Most commonly affecting middle-aged and older people, OA can range from very mild to very severe. It affects hands and weight-bearing joints such as knees, hips, feet and the back. Knee OA can be as disabling as any cardiovascular disease except stroke.

[0013] Osteoarthritis affects an estimated 20.7 million Americans, mostly after age 45, with women more commonly affected than men. Physicians make a diagnosis of OA based on a physical exam and history of symptoms. X-rays are used to confirm diagnosis. Most people over 60 reflect the disease on X-ray, and about one-third have actual symptoms.

[0014] There are many factors that can cause OA. Obesity may lead to osteoarthritis of the knees. In addition, people with joint injuries due to sports, work-related activity or accidents may be at increased risk of developing OA.

[0015] Genetics has a role in the development of OA. Some people may be born with defective cartilage or with slight defects in the way that joints fit together. As a person ages, these defects may

cause early cartilage breakdown in the joint or the inability to repair damaged or deteriorated cartilage in the joint.

[0016] Inclusion or exclusion of samples for an osteoarthritis pool may be based upon the following criteria: ethnicity (e.g., samples derived from an individual characterized as Caucasian); parental ethnicity (e.g., samples derived from an individual of British paternal and maternal descent); relevant phenotype information for the individual (e.g., case samples derived from individuals diagnosed with specific knee osteoarthritis (OA) and were recruited from an OA knee replacement clinic). Control samples may be selected based on relevant phenotype information for the individual (e.g., derived from individuals free of OA at several sites (knee, hand, hip etc)); and no family history of OA and/or rheumatoid arthritis. Additional phenotype information collected for both cases and controls may include age of the individual, gender, family history of OA, diagnosis with osteoarthritis (joint location of OA, date of primary diagnosis, age of individual as of primary diagnosis), knee history (current symptoms, any major knee injury, meniscectomy, knee replacement surgery, age of surgery), HRT history, osteoporosis diagnosis.

[0017] Based in part upon selection criteria set forth above, individuals having osteoarthritis can be selected for genetic studies. Also, individuals having no history of osteoarthritis often are selected for genetic studies, as described hereafter.

Polymorphic Variants Associated with Osteoarthritis

[0018] A genetic analysis provided herein linked osteoarthritis with polymorphic variant nucleic acid sequences in the human genome. As used herein, the term “polymorphic site” refers to a region in a nucleic acid at which two or more alternative nucleotide sequences are observed in a significant number of nucleic acid samples from a population of individuals. A polymorphic site may be a nucleotide sequence of two or more nucleotides, an inserted nucleotide or nucleotide sequence, a deleted nucleotide or nucleotide sequence, or a microsatellite, for example. A polymorphic site that is two or more nucleotides in length may be 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more, 20 or more, 30 or more, 50 or more, 75 or more, 100 or more, 500 or more, or about 1000 nucleotides in length, where all or some of the nucleotide sequences differ within the region. A polymorphic site is often one nucleotide in length, which is referred to herein as a “single nucleotide polymorphism” or a “SNP.”

[0019] Where there are two, three, or four alternative nucleotide sequences at a polymorphic site, each nucleotide sequence is referred to as a “polymorphic variant” or “nucleic acid variant.” Where two polymorphic variants exist, for example, the polymorphic variant represented in a minority of samples from a population is sometimes referred to as a “minor allele” and the polymorphic variant that is more prevalently represented is sometimes referred to as a “major allele.” Many organisms possess a copy of each chromosome (e.g., humans), and those individuals who possess two major alleles or two minor

alleles are often referred to as being “homozygous” with respect to the polymorphism, and those individuals who possess one major allele and one minor allele are normally referred to as being “heterozygous” with respect to the polymorphism. Individuals who are homozygous with respect to one allele are sometimes predisposed to a different phenotype as compared to individuals who are heterozygous or homozygous with respect to another allele.

[0020] In genetic analysis that associate polymorphic variants with osteoarthritis, samples from individuals having osteoarthritis and individuals not having osteoarthritis often are allelotyped and/or genotyped. The term “allelotype” as used herein refers to a process for determining the allele frequency for a polymorphic variant in pooled DNA samples from cases and controls. By pooling DNA from each group, an allele frequency for each SNP in each group is calculated. These allele frequencies are then compared to one another. The term “genotyped” as used herein refers to a process for determining a genotype of one or more individuals, where a “genotype” is a representation of one or more polymorphic variants in a population.

[0021] A genotype or polymorphic variant may be expressed in terms of a “haplotype,” which as used herein refers to two or more polymorphic variants occurring within genomic DNA in a group of individuals within a population. For example, two SNPs may exist within a gene where each SNP position includes a cytosine variation and an adenine variation. Certain individuals in a population may carry one allele (heterozygous) or two alleles (homozygous) having the gene with a cytosine at each SNP position. As the two cytosines corresponding to each SNP in the gene travel together on one or both alleles in these individuals, the individuals can be characterized as having a cytosine/cytosine haplotype with respect to the two SNPs in the gene.

[0022] As used herein, the term “phenotype” refers to a trait which can be compared between individuals, such as presence or absence of a condition, a visually observable difference in appearance between individuals, metabolic variations, physiological variations, variations in the function of biological molecules, and the like. An example of a phenotype is occurrence of osteoarthritis.

[0023] Researchers sometimes report a polymorphic variant in a database without determining whether the variant is represented in a significant fraction of a population. Because a subset of these reported polymorphic variants are not represented in a statistically significant portion of the population, some of them are sequencing errors and/or not biologically relevant. Thus, it is often not known whether a reported polymorphic variant is statistically significant or biologically relevant until the presence of the variant is detected in a population of individuals and the frequency of the variant is determined. Methods for detecting a polymorphic variant in a population are described herein, specifically in Example 2. A polymorphic variant is statistically significant and often biologically relevant if it is represented in 5% or more of a population, sometimes 10% or more, 15% or more, or 20% or more of a population, and often 25% or more, 30% or more, 35% or more, 40% or more, 45% or more, or 50% or more of a population.

[0024] A polymorphic variant may be detected on either or both strands of a double-stranded nucleic acid. Also, a polymorphic variant may be located within an intron or exon of a gene or within a portion of a regulatory region such as a promoter, a 5' untranslated region (UTR), a 3' UTR, and in DNA (*e.g.*, genomic DNA (gDNA) and complementary DNA (cDNA)), RNA (*e.g.*, mRNA, tRNA, and rRNA), or a polypeptide. Polymorphic variations may or may not result in detectable differences in gene expression, polypeptide structure, or polypeptide function.

[0025] It was determined that polymorphic variations associated with an increased risk of osteoarthritis existed in SEQ ID NO: 1-3 or a nucleotide sequence referenced in Table A. In certain embodiments, polymorphic variants at positions rs552, rs12904, rs2282146, rs734784, rs1042164, rs749670, rs955592, rs1143016, rs755248, rs1055055, rs835409, rs927663, rs8162, rs831038, rs33079, rs1710880, rs4472029, rs799570, rs1282730, rs1518875, rs1568694, rs905042, rs1957723, rs794018, rs707723, rs893861, rs1914903, rs2062232, rs26609, rs1370987, rs1012414, rs435903, rs1248, rs703508, rs226465, rs241448, rs763155, rs1040461, rs462832, rs804194, rs1022646, rs1569112, rs805623, rs1019850, rs1599931, AA, rs279941, rs1062230, rs1859911, rs1477261, rs1191119, rs657780, rs1393890, rs1478714, rs868213, rs690115, rs1465501, rs899173, rs10477, rs926393, rs465271, rs13847 and/or rs738658 in the human genome were associated with an increased risk of osteoarthritis, and in specific embodiments, the corresponding allele in the right-most column in Table A for each position is associated with an increased risk of osteoarthritis. In other embodiments polymorphic variants at positions rs734784, rs1042164, rs749670, rs955592 and rs1040461 were associated with an increased risk of osteoarthritis, and in specific embodiments, a valine encoded by rs734784, a valine encoded by rs1042164, a glutamate encoded by rs749670, a threonine encoded by rs955592 and a glycine encoded by rs1040461 were associated with an increased risk of osteoarthritis.

[0026] Polymorphic variants in and around the *KIAA0296* locus were tested for association with osteoarthritis. These include polymorphic variants at positions in SEQ ID NO: 1 selected from the group consisting of 247, 1535, 2386, 6440, 9133, 9143, 9471, 13150, 13717, 14466, 15769, 16870, 18545, 18749, 19123, 20736, 21038, 21046, 21050, 21056, 21706, 23170, 25028, 27871, 28070, 31717, 32019, 32318, 33080, 33101, 34236, 34285, 34818, 35168, 37981, 38113, 38117, 38481, 38615, 38944, 39288, 41385, 42136, 42185, 42353, 42434, 44580, 44675, 45739, 46439, 47457, 47735, 50319, 50708, 51185, 53002, 53064, 53637, 55274, 55825, 55986, 56684, 57653, 57659, 57692, 57775, 61313, 61431, 61699, 62906, 63619, 64664, 68452, 69665, 69681, 70091, 74637, 74760, 76523, 78559, 79549, 79882, 81339, 81681, 81696, 83517, 85431, 86332, 87358, 87725, 89052, 90020, 90231, 90284, 90447, 90601, 90724, 92559, 95176, 95195 and 96822. Polymorphic variants at the following positions in SEQ ID NO: 1 in particular were associated with an increased risk of osteoarthritis: 13150, 21046, 23170, 25028, 44580, 62906, 64664 and 83517. In particular, the following polymorphic variants in SEQ ID NO: 1 were associated with risk of osteoarthritis: a guanine at position 13150, a thymine at position 21046, an

adenine at position 23170, an adenine at position 25028, a guanine at position 44580, a guanine at position 62906, a cytosine at position 64664 and a cytosine at position 83517. A polymorphic variant in a *KIAA0296* polypeptide encoded by rs749670 (e.g., a glutamate at position 327 in the polypeptide) also was associated with increased risk of osteoarthritis.

[0027] Polymorphic variants in and around the *chrom 4* locus were tested for association with osteoarthritis. These include polymorphic variants at positions in SEQ ID NO: 2 selected from the group consisting of 211, 7217, 7895, 13308, 14279, 17026, 18271, 20417, 21843, 22069, 22145, 22519, 22539, 23236, 23256, 23402, 23499, 23620, 23871, 24136, 25427, 25866, 26541, 26576, 26689, 26720, 27113, 27164, 27186, 28341, 29160, 29844, 30665, 30830, 31061, 31523, 32326, 32346, 32358, 34909, 34975, 35066, 35096, 35375, 36304, 36712, 36770, 37342, 37412, 37884, 38077, 38300, 38301, 41189, 44408, 44493, 44571, 44670, 45219, 45258, 47261, 48473, 48771, 55292, 56479, 56747, 60620, 60688, 61058, 61129, 61577, 61961, 63351, 63926, 65798, 66043, 66044, 66246, 66318, 66547, 71238, 71283, 71492, 72274, 73762, 74209, 75284, 77347, 77589, 78096, 78606, 78862, 79135, 79146, 79456, 79609, 80086, 80119, 80766, 81110, 81269, 81668, 82433, 82559, 83298, 83821, 84121, 84147, 84543, 84554, 84691, 84727, 85678, 86699, 86700, 86792, 86832, 87045, 87140, 87365, 88342, 88498, 88589, 95502, 96968, 97448, 97568 and 98724. Polymorphic variants at the following positions in SEQ ID NO: 2 in particular were associated with an increased risk of osteoarthritis: 23236, 32358, 47261, 48771, 55292, 60688, 72274, 74209, 77589, 79135, 79456, 79609, 80119, 80766, 81110, 82433, 84121, 84147, 85678, 86699, 86832, 87140 and 88589, where specific embodiments are directed to a polymorphic variant at position 32358, 47261, 74209 and/or 79456. In particular, the following polymorphic variants in SEQ ID NO: 2 were associated with risk of osteoarthritis: an adenine at position 23236, a cytosine at position 32358, a guanine at position 47261, a guanine at position 48771, a cytosine at position 55292, an adenine at position 60688, a guanine at position 72274, a guanine at position 74209, a cytosine at position 77589, an adenine at position 79135, a thymine at position 79456, an adenine at position 79609, an adenine at position 80119, a cytosine at position 80766, an adenine at position 81110, a cytosine at position 82433, a cytosine at position 84121, a thymine at position 84147, a cytosine at position 85678, a thymine at position 86699, an adenine at position 86832, a guanine at position 87140 and an adenine at position 88589.

[0028] Polymorphic variants in and around the *SNW1* locus were tested for association with osteoarthritis. These include polymorphic variants at positions in SEQ ID NO: 3 selected from the group consisting of 218, 1440, 1442, 2611, 4317, 4724, 4788, 5202, 5780, 5974, 6644, 7430, 7938, 8095, 8183, 8312, 8352, 9348, 9378, 9617, 9727, 9834, 9899, 10211, 10377, 10695, 10729, 10730, 11433, 11951, 12697, 12982, 14419, 14501, 14983, 15280, 15475, 15888, 15976, 16307, 16442, 17255, 18948, 19435, 19753, 20021, 20022, 20503, 20590, 21804, 21919, 21990, 22412, 22536, 23432, 23468, 23772, 24325, 24773, 26274, 27440, 28561, 30071, 31764, 33008, 35310, 35460, 37112, 37285, 37747, 38057, 38859,

38860, 39525, 40216, 40281, 41453, 42091, 42513, 42935, 42985, 43003, 43281, 43716, 43866, 44234, 44596, 44871, 45005, 45282, 47178, 47816, 47887, 48134, 48135, 48276, 48400, 48798, 48803, 49146, 49969, 51059, 51064, 53285, 54560, 54748, 54785, 55102, 55644, 55705, 55841, 56623, 56825, 56827, 56892, 59150, 59958, 60231, 60524, 61871, 62226, 63230, 63468, 63787, 65732, 65989, 68832, 69904, 70365, 70886, 73088, 73103, 75934, 75966, 76273, 77943, 78466, 78861, 78872, 79836, 80908, 81509, 83576, 83662, 83782, 84282, 84444, 85129, 85151, 85296, 85809, 86387, 86494, 89786, 89894, 90122, 92067, 92187, 92312, 92824, 93733, 96553 and 96941. Polymorphic variants at the following positions in SEQ ID NO: 3 in particular were associated with an increased risk of osteoarthritis: 4788, 8312, 9378, 9727, 9899, 10211, 27440, 40216, 40281, 42091, 43866, 48803, 51059, 55644, 56623, 73103, 78872, 79836, 85129, 92824 and 96941. In particular, the following polymorphic variants in SEQ ID NO: 3 were associated with risk of osteoarthritis: a guanine at position 4788, a thymine at position 8312, a deletion at position 9378, a cytosine at position 9727, a guanine at position 9899, a cytosine at position 10211, a guanine at position 27440, a guanine at position 40216, a cytosine at position 40281, an adenine at position 42091, a guanine at position 43866, an adenine at position 48803, an adenine at position 51059, an adenine at position 55644, a cytosine at position 56623, a cytosine at position 73103, an adenine at position 78872, a guanine at position 79836, a cytosine at position 85129, a guanine at position 92824 and an adenine at position 96941.

[0029] Based in part upon analyses summarized in Figures 1A-1C, regions with significant association have been identified in regions associated with osteoarthritis. Any polymorphic variants associated with osteoarthritis in a region of significant association can be utilized for embodiments described herein. For example, polymorphic variants in a region spanning chromosome positions 31118000 to 31129000 (approximately 11,000 nucleotides in length) in a *KIAA0296* locus, a region spanning chromosome positions 36914000 to 36931000 (approximately 17,000 nucleotides in length) in a *chrom 4* locus and a region spanning chromosome positions 76196500 to 76221500 (approximately 25,000 nucleotides in length) in a *SNWI* locus have significant association (chromosome positions are within NCBI's Genome build 34).

Additional Polymorphic Variants Associated with Osteoarthritis

[0030] Also provided is a method for identifying polymorphic variants proximal to an incident, founder polymorphic variant associated with osteoarthritis. Thus, featured herein are methods for identifying a polymorphic variation associated with osteoarthritis that is proximal to an incident polymorphic variation associated with osteoarthritis, which comprises identifying a polymorphic variant proximal to the incident polymorphic variant associated with osteoarthritis, where the incident polymorphic variant is in a *KIAA0296*, *chrom 4* or *SNWI* nucleotide sequence or other nucleotide sequence referenced in Table A. The nucleotide sequence often comprises a polynucleotide sequence

selected from the group consisting of (a) a polynucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A; (b) a polynucleotide sequence that encodes a polypeptide having an amino acid sequence encoded by a polynucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A; and (c) a polynucleotide sequence that encodes a polypeptide having an amino acid sequence that is 90% or more identical to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A or a polynucleotide sequence 90% or more identical to the polynucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A. The presence or absence of an association of the proximal polymorphic variant with osteoarthritis then is determined using a known association method, such as a method described in the Examples hereafter. In an embodiment, the incident polymorphic variant is a polymorphic variant associated with osteoarthritis described herein. In another embodiment, the proximal polymorphic variant identified sometimes is a publicly disclosed polymorphic variant, which for example, sometimes is published in a publicly available database. In other embodiments, the polymorphic variant identified is not publicly disclosed and is discovered using a known method, including, but not limited to, sequencing a region surrounding the incident polymorphic variant in a group of nucleic acid samples. Thus, multiple polymorphic variants proximal to an incident polymorphic variant are associated with osteoarthritis using this method.

[0031] The proximal polymorphic variant often is identified in a region surrounding the incident polymorphic variant. In certain embodiments, this surrounding region is about 50 kb flanking the first polymorphic variant (*e.g.* about 50 kb 5' of the first polymorphic variant and about 50 kb 3' of the first polymorphic variant), and the region sometimes is composed of shorter flanking sequences, such as flanking sequences of about 40 kb, about 30 kb, about 25 kb, about 20 kb, about 15 kb, about 10 kb, about 7 kb, about 5 kb, or about 2 kb 5' and 3' of the incident polymorphic variant. In other embodiments, the region is composed of longer flanking sequences, such as flanking sequences of about 55 kb, about 60 kb, about 65 kb, about 70 kb, about 75 kb, about 80 kb, about 85 kb, about 90 kb, about 95 kb, or about 100 kb 5' and 3' of the incident polymorphic variant.

[0032] In certain embodiments, polymorphic variants associated with osteoarthritis are identified iteratively. For example, a first proximal polymorphic variant is associated with osteoarthritis using the methods described above and then another polymorphic variant proximal to the first proximal polymorphic variant is identified (*e.g.*, publicly disclosed or discovered) and the presence or absence of an association of one or more other polymorphic variants proximal to the first proximal polymorphic variant with osteoarthritis is determined.

[0033] The methods described herein are useful for identifying or discovering additional polymorphic variants that may be used to further characterize a gene, region or loci associated with a condition, a disease (*e.g.*, osteoarthritis), or a disorder. For example, allelotyping or genotyping data from the additional polymorphic variants may be used to identify a functional mutation or a region of

linkage disequilibrium. In certain embodiments, polymorphic variants identified or discovered within a region comprising the first polymorphic variant associated with osteoarthritis are genotyped using the genetic methods and sample selection techniques described herein, and it can be determined whether those polymorphic variants are in linkage disequilibrium with the first polymorphic variant. The size of the region in linkage disequilibrium with the first polymorphic variant also can be assessed using these genotyping methods. Thus, provided herein are methods for determining whether a polymorphic variant is in linkage disequilibrium with a first polymorphic variant associated with osteoarthritis, and such information can be used in prognosis/diagnosis methods described herein.

Isolated Nucleic Acids

[0034] Featured herein are isolated *KIAA0296*, *chrom 4* or *SNW1* nucleic acid variants depicted in SEQ ID NO: 1-3 or referenced in Table A, and substantially identical nucleic acids thereof. A nucleic acid variant may be represented on one or both strands in a double-stranded nucleic acid or on one chromosomal complement (heterozygous) or both chromosomal complements (homozygous).

[0035] As used herein, the term “nucleic acid” includes DNA molecules (*e.g.*, a complementary DNA (cDNA) and genomic DNA (gDNA)) and RNA molecules (*e.g.*, mRNA, rRNA, siRNA and tRNA) and analogs of DNA or RNA, for example, by use of nucleotide analogs. The nucleic acid molecule can be single-stranded and it is often double-stranded. The term “isolated or purified nucleic acid” refers to nucleic acids that are separated from other nucleic acids present in the natural source of the nucleic acid. For example, with regard to genomic DNA, the term “isolated” includes nucleic acids which are separated from the chromosome with which the genomic DNA is naturally associated. An “isolated” nucleic acid is often free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5’ and/or 3’ ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of 5’ and/or 3’ nucleotide sequences which flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an “isolated” nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. As used herein, the term “gene” refers to a nucleotide sequence that encodes a polypeptide.

[0036] Also included herein are nucleic acid fragments. These fragments often have a nucleotide sequence identical to a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A, a nucleotide sequence substantially identical to a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A, or a nucleotide sequence that is complementary to the foregoing. The nucleic acid fragment may be identical, substantially identical or homologous to a nucleotide sequence in an exon or an intron in a

nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A, and may encode a domain or part of a domain of a polypeptide. Sometimes, the fragment will comprises one or more of the polymorphic variations described herein as being associated with osteoarthritis. The nucleic acid fragment is often 50, 100, or 200 or fewer base pairs in length, and is sometimes about 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 2000, 3000, 4000, 5000, 10000, 15000, or 20000 base pairs in length. A nucleic acid fragment that is complementary to a nucleotide sequence identical or substantially identical to a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A and hybridizes to such a nucleotide sequence under stringent conditions is often referred to as a "probe." Nucleic acid fragments often include one or more polymorphic sites, or sometimes have an end that is adjacent to a polymorphic site as described hereafter.

[0037] An example of a nucleic acid fragment is an oligonucleotide. As used herein, the term "oligonucleotide" refers to a nucleic acid comprising about 8 to about 50 covalently linked nucleotides, often comprising from about 8 to about 35 nucleotides, and more often from about 10 to about 25 nucleotides. The backbone and nucleotides within an oligonucleotide may be the same as those of naturally occurring nucleic acids, or analogs or derivatives of naturally occurring nucleic acids, provided that oligonucleotides having such analogs or derivatives retain the ability to hybridize specifically to a nucleic acid comprising a targeted polymorphism. Oligonucleotides described herein may be used as hybridization probes or as components of prognostic or diagnostic assays, for example, as described herein.

[0038] Oligonucleotides are typically synthesized using standard methods and equipment, such as the ABI™3900 High Throughput DNA Synthesizer and the EXPEDITE™ 8909 Nucleic Acid Synthesizer, both of which are available from Applied Biosystems (Foster City, CA). Analogs and derivatives are exemplified in U.S. Pat. Nos. 4,469,863; 5,536,821; 5,541,306; 5,637,683; 5,637,684; 5,700,922; 5,717,083; 5,719,262; 5,739,308; 5,773,601; 5,886,165; 5,929,226; 5,977,296; 6,140,482; WO 00/56746; WO 01/14398, and related publications. Methods for synthesizing oligonucleotides comprising such analogs or derivatives are disclosed, for example, in the patent publications cited above and in U.S. Pat. Nos. 5,614,622; 5,739,314; 5,955,599; 5,962,674; 6,117,992; in WO 00/75372; and in related publications.

[0039] Oligonucleotides may also be linked to a second moiety. The second moiety may be an additional nucleotide sequence such as a tail sequence (*e.g.*, a polyadenosine tail), an adapter sequence (*e.g.*, phage M13 universal tail sequence), and others. Alternatively, the second moiety may be a non-nucleotide moiety such as a moiety which facilitates linkage to a solid support or a label to facilitate detection of the oligonucleotide. Such labels include, without limitation, a radioactive label, a fluorescent label, a chemiluminescent label, a paramagnetic label, and the like. The second moiety may

be attached to any position of the oligonucleotide, provided the oligonucleotide can hybridize to the nucleic acid comprising the polymorphism.

Uses for Nucleic Acid Sequence

[0040] Nucleic acid coding sequences may be used for diagnostic purposes for detection and control of polypeptide expression. Also, included herein are oligonucleotide sequences such as antisense RNA, small-interfering RNA (siRNA) and DNA molecules and ribozymes that function to inhibit translation of a polypeptide. Antisense techniques and RNA interference techniques are known in the art and are described herein.

[0041] Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, hammerhead motif ribozyme molecules may be engineered that specifically and efficiently catalyze endonucleolytic cleavage of RNA sequences corresponding to or complementary to *KIAA0296, chrom 4* or *SNW1* nucleotide sequences or other nucleotide sequences referenced in Table A. Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites which include the following sequences, GUA, GUU and GUC. Once identified, short RNA sequences of between fifteen (15) and twenty (20) ribonucleotides corresponding to the region of the target gene containing the cleavage site may be evaluated for predicted structural features such as secondary structure that may render the oligonucleotide sequence unsuitable. The suitability of candidate targets may also be evaluated by testing their accessibility to hybridization with complementary oligonucleotides, using ribonuclease protection assays.

[0042] Antisense RNA and DNA molecules, siRNA and ribozymes may be prepared by any method known in the art for the synthesis of RNA molecules. These include techniques for chemically synthesizing oligodeoxyribonucleotides well known in the art such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors which incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

[0043] DNA encoding a polypeptide also may have a number of uses for the diagnosis of diseases, including osteoarthritis, resulting from aberrant expression of a target gene described herein. For example, the nucleic acid sequence may be used in hybridization assays of biopsies or autopsies to diagnose abnormalities of expression or function (*e.g.*, Southern or Northern blot analysis, *in situ* hybridization assays).

[0044] In addition, the expression of a polypeptide during embryonic development may also be determined using nucleic acid encoding the polypeptide. As addressed, *infra*, production of functionally impaired polypeptide is the cause of various disease states, such as osteoarthritis. *In situ* hybridizations using polypeptide as a probe may be employed to predict problems related to osteoarthritis. Further, as indicated, *infra*, administration of human active polypeptide, recombinantly produced as described herein, may be used to treat disease states related to functionally impaired polypeptide. Alternatively, gene therapy approaches may be employed to remedy deficiencies of functional polypeptide or to replace or compete with dysfunctional polypeptide.

Expression Vectors, Host Cells, and Genetically Engineered Cells

[0045] Provided herein are nucleic acid vectors, often expression vectors, which contain a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A, or a substantially identical sequence thereof. As used herein, the term “vector” refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked and can include a plasmid, cosmid, or viral vector. The vector can be capable of autonomous replication or it can integrate into a host DNA. Viral vectors may include replication defective retroviruses, adenoviruses and adeno-associated viruses for example.

[0046] A vector can include a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A in a form suitable for expression of an encoded target polypeptide or target nucleic acid in a host cell. A “target polypeptide” is a polypeptide encoded by a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A, or a substantially identical nucleotide sequence thereof. The recombinant expression vector typically includes one or more regulatory sequences operatively linked to the nucleic acid sequence to be expressed. The term “regulatory sequence” includes promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence, as well as tissue-specific regulatory and/or inducible sequences. The design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of polypeptide desired, and the like. Expression vectors can be introduced into host cells to produce target polypeptides, including fusion polypeptides.

[0047] Recombinant expression vectors can be designed for expression of target polypeptides in prokaryotic or eukaryotic cells. For example, target polypeptides can be expressed in *E. coli*, insect cells (*e.g.*, using baculovirus expression vectors), yeast cells, or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology 185*, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

[0048] Expression of polypeptides in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion polypeptides. Fusion vectors add a number of amino acids to a polypeptide encoded therein, usually to the amino terminus of the recombinant polypeptide. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant polypeptide; 2) to increase the solubility of the recombinant polypeptide; and 3) to aid in the purification of the recombinant polypeptide by acting as a ligand in affinity purification. Often, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant polypeptide to enable separation of the recombinant polypeptide from the fusion moiety subsequent to purification of the fusion polypeptide. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith & Johnson, *Gene* 67: 31-40 (1988)), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding polypeptide, or polypeptide A, respectively, to the target recombinant polypeptide.

[0049] Purified fusion polypeptides can be used in screening assays and to generate antibodies specific for target polypeptides. In a therapeutic embodiment, fusion polypeptide expressed in a retroviral expression vector is used to infect bone marrow cells that are subsequently transplanted into irradiated recipients. The pathology of the subject recipient is then examined after sufficient time has passed (*e.g.*, six (6) weeks).

[0050] Expressing the polypeptide in host bacteria with an impaired capacity to proteolytically cleave the recombinant polypeptide is often used to maximize recombinant polypeptide expression (Gottesman, S., *Gene Expression Technology: Methods in Enzymology*, Academic Press, San Diego, California 185: 119-128 (1990)). Another strategy is to alter the nucleotide sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, *Nucleic Acids Res.* 20: 2111-2118 (1992)). Such alteration of nucleotide sequences can be carried out by standard DNA synthesis techniques.

[0051] When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. Recombinant mammalian expression vectors are often capable of directing expression of the nucleic acid in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Non-limiting examples of suitable tissue-specific promoters include an albumin promoter (liver-specific; Pinkert *et al.*, *Genes Dev.* 1: 268-277 (1987)), lymphoid-specific promoters (Calame & Eaton, *Adv. Immunol.* 43: 235-275 (1988)), promoters of T cell receptors (Winoto & Baltimore, *EMBO J.* 8: 729-733 (1989)) promoters of immunoglobulins (Banerji *et al.*, *Cell* 33: 729-740 (1983); Queen & Baltimore, *Cell* 33: 741-748 (1983)), neuron-specific

promoters (*e.g.*, the neurofilament promoter; Byrne & Ruddle, *Proc. Natl. Acad. Sci. USA* 86: 5473-5477 (1989)), pancreas-specific promoters (Edlund *et al.*, *Science* 230: 912-916 (1985)), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are sometimes utilized, for example, the murine hox promoters (Kessel & Gruss, *Science* 249: 374-379 (1990)) and the α -fetopolypeptide promoter (Campes & Tilghman, *Genes Dev.* 3: 537-546 (1989)).

[0052] A *KIAA0296*, *chrom 4* or *SNW1* nucleic acid or other nucleic acid referenced in Table A also may be cloned into an expression vector in an antisense orientation. Regulatory sequences (*e.g.*, viral promoters and/or enhancers) operatively linked to a *KIAA0296*, *chrom 4* or *SNW1* nucleic acid or other nucleic acid referenced in Table A cloned in the antisense orientation can be chosen for directing constitutive, tissue specific or cell type specific expression of antisense RNA in a variety of cell types. Antisense expression vectors can be in the form of a recombinant plasmid, phagemid or attenuated virus. For a discussion of the regulation of gene expression using antisense genes *see, e.g.*, Weintraub *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) (1986).

[0053] Also provided herein are host cells that include a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A within a recombinant expression vector or a fragment of such a nucleotide sequence which facilitate homologous recombination into a specific site of the host cell genome. The terms "host cell" and "recombinant host cell" are used interchangeably herein. Such terms refer not only to the particular subject cell but rather also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein. A host cell can be any prokaryotic or eukaryotic cell. For example, a target polypeptide can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

[0054] Vectors can be introduced into host cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, transduction/infection, DEAE-dextran-mediated transfection, lipofection, or electroporation.

[0055] A host cell provided herein can be used to produce (*i.e.*, express) a target polypeptide or a substantially identical polypeptide thereof. Accordingly, further provided are methods for producing a target polypeptide using host cells described herein. In one embodiment, the method includes culturing host cells into which a recombinant expression vector encoding a target polypeptide has been introduced

in a suitable medium such that a target polypeptide is produced. In another embodiment, the method further includes isolating a target polypeptide from the medium or the host cell.

[0056] Also provided are cells or purified preparations of cells which include a *KIAA0296, chrom 4* or *SNW1* transgene, or other transgene in Table A, or which otherwise misexpress target polypeptide. Cell preparations can consist of human or non-human cells, *e.g.*, rodent cells, *e.g.*, mouse or rat cells, rabbit cells, or pig cells. In preferred embodiments, the cell or cells include a *KIAA0296, chrom 4* or *SNW1* transgene or other transgene referenced in Table A (*e.g.*, a heterologous form of a *KIAA0296, chrom 4* or *SNW1* gene or other gene referenced in Table A, such as a human gene expressed in non-human cells). The transgene can be misexpressed, *e.g.*, overexpressed or underexpressed. In other preferred embodiments, the cell or cells include a gene which misexpress an endogenous target polypeptide (*e.g.*, expression of a gene is disrupted, also known as a knockout). Such cells can serve as a model for studying disorders which are related to mutated or mis-expressed alleles or for use in drug screening. Also provided are human cells (*e.g.*, a hematopoietic stem cells) transfected with a *KIAA0296, chrom 4* or *SNW1* nucleic acid or other nucleic acid referenced in Table A.

[0057] Also provided are cells or a purified preparation thereof (*e.g.*, human cells) in which an endogenous *KIAA0296, chrom 4* or *SNW1* nucleic acid or other nucleic acid referenced in Table A is under the control of a regulatory sequence that does not normally control the expression of the endogenous gene. The expression characteristics of an endogenous gene within a cell (*e.g.*, a cell line or microorganism) can be modified by inserting a heterologous DNA regulatory element into the genome of the cell such that the inserted regulatory element is operably linked to the corresponding endogenous gene. For example, an endogenous corresponding gene (*e.g.*, a gene which is “transcriptionally silent,” not normally expressed, or expressed only at very low levels) may be activated by inserting a regulatory element which is capable of promoting the expression of a normally expressed gene product in that cell. Techniques such as targeted homologous recombinations, can be used to insert the heterologous DNA as described in, *e.g.*, Chappel, US 5,272,071; WO 91/06667, published on May 16, 1991.

Transgenic Animals

[0058] Non-human transgenic animals that express a heterologous target polypeptide (*e.g.*, expressed from a *KIAA0296, chrom 4* or *SNW1* nucleic acid or other nucleic acid referenced in Table A, or substantially identical sequence thereof) can be generated. Such animals are useful for studying the function and/or activity of a target polypeptide and for identifying and/or evaluating modulators of the activity of *KIAA0296, chrom 4* or *SNW1* nucleic acids, other nucleic acids referenced in Table A, and encoded polypeptides. As used herein, a “transgenic animal” is a non-human animal such as a mammal (*e.g.*, a non-human primate such as chimpanzee, baboon, or macaque; an ungulate such as an equine, bovine, or caprine; or a rodent such as a rat, a mouse, or an Israeli sand rat), a bird (*e.g.*, a chicken or a

turkey), an amphibian (*e.g.*, a frog, salamander, or newt), or an insect (*e.g.*, *Drosophila melanogaster*), in which one or more of the cells of the animal includes a transgene. A transgene is exogenous DNA or a rearrangement (*e.g.*, a deletion of endogenous chromosomal DNA) that is often integrated into or occurs in the genome of cells in a transgenic animal. A transgene can direct expression of an encoded gene product in one or more cell types or tissues of the transgenic animal, and other transgenes can reduce expression (*e.g.*, a knockout). Thus, a transgenic animal can be one in which an endogenous nucleic acid homologous to a *KIAA0296*, *chrom 4* or *SNWI* nucleic acid or other nucleic acid referenced in Table A has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal (*e.g.*, an embryonic cell of the animal) prior to development of the animal.

[0059] Intronic sequences and polyadenylation signals can also be included in the transgene to increase expression efficiency of the transgene. One or more tissue-specific regulatory sequences can be operably linked to a *KIAA0296*, *chrom 4* or *SNWI* nucleotide sequence or other nucleotide sequence referenced in Table A to direct expression of an encoded polypeptide to particular cells. A transgenic founder animal can be identified based upon the presence of a *KIAA0296*, *chrom 4* or *SNWI* nucleotide sequence or other nucleotide sequence referenced in Table A in its genome and/or expression of encoded mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a *KIAA0296*, *chrom 4* or *SNWI* nucleotide sequence or other nucleotide sequence referenced in Table A can further be bred to other transgenic animals carrying other transgenes.

[0060] Target polypeptides can be expressed in transgenic animals or plants by introducing, for example, a *KIAA0296*, *chrom 4* or *SNWI* nucleic acid or other nucleic acid referenced in Table A into the genome of an animal that encodes the target polypeptide. In preferred embodiments the nucleic acid is placed under the control of a tissue specific promoter, *e.g.*, a milk or egg specific promoter, and recovered from the milk or eggs produced by the animal. Also included is a population of cells from a transgenic animal.

Target Polypeptides

[0061] Also featured herein are isolated target polypeptides, which are encoded by a *KIAA0296*, *chrom 4* or *SNWI* nucleotide sequence or a nucleotide sequence referenced in Table A (*e.g.*, SEQ ID NO: 1-3 or a sequence referenced in Table A), or a substantially identical nucleotide sequence thereof. The term “polypeptide” as used herein includes proteins and peptides. An “isolated” or “purified” polypeptide or protein is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. In one embodiment, the language “substantially free”

means preparation of a target polypeptide having less than about 30%, 20%, 10% and more preferably 5% (by dry weight), of non-target polypeptide (also referred to herein as a “contaminating protein”), or of chemical precursors or non-target chemicals. When the target polypeptide or a biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, specifically, where culture medium represents less than about 20%, sometimes less than about 10%, and often less than about 5% of the volume of the polypeptide preparation. Isolated or purified target polypeptide preparations are sometimes 0.01 milligrams or more or 0.1 milligrams or more, and often 1.0 milligrams or more and 10 milligrams or more in dry weight.

[0062] Further included herein are target polypeptide fragments. The polypeptide fragment may be a domain or part of a domain of a target polypeptide. The polypeptide fragment may have increased, decreased or unexpected biological activity. The polypeptide fragment is often 50 or fewer, 100 or fewer, or 200 or fewer amino acids in length, and is sometimes 300, 400, 500, 600, 700, or 900 or fewer amino acids in length. Specific embodiments are directed to a *PTPNI* polypeptide fragment (e.g., rs2282146 in Table A), such as a catalytic domain starting at about amino acid 3 and ending at about amino acid 279. Other embodiments are directed to a *KCNS1* polypeptide fragment (e.g., rs734784 in Table A), such as a voltage gated postassium ion channel domain (e.g., starting at about amino acid 21 and ending at about amino acid 509), a postassium channel tetramerization domain (e.g., starting at about amino acid 52 and ending at about amino acid 155) or an ion transport protein domain (e.g., starting at about amino acid 271 and ending at about amino acid 456), for example. Certain embodiments are directed to a *ANXA6* polypeptide fragment (e.g., rs1012414 in Table A), such as an annexin domain starting at about amino acid 5 and ending at about amino acid 325, an annexin domain starting at about amino acid 179 and ending at about amino acid 507, or an annexin domain starting at about amino acid 355 and ending at about amino acid 673 in isoform 1 or isoform 2 (e.g., an isoform 1 sequence can be accessed using accession number NP_001146 and an isoform 2 sequence can be accessed using accession number NP_004024; isoform 2 lacks exon 21 and encodes a protein isoform lacking the six amino acids VAAEIL). Amino acid sequences can be accessed using information in Table A.

[0063] Substantially identical target polypeptides may depart from the amino acid sequences of target polypeptides in different manners. For example, conservative amino acid modifications may be introduced at one or more positions in the amino acid sequences of target polypeptides. A “conservative amino acid substitution” is one in which the amino acid is replaced by another amino acid having a similar structure and/or chemical function. Families of amino acid residues having similar structures and functions are well known. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side

chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Also, essential and non-essential amino acids may be replaced. A “non-essential” amino acid is one that can be altered without abolishing or substantially altering the biological function of a target polypeptide, whereas altering an “essential” amino acid abolishes or substantially alters the biological function of a target polypeptide. Amino acids that are conserved among target polypeptides are typically essential amino acids. In certain embodiments, the polypeptide includes one or more non-synonymous polymorphic variants associated with osteoarthritis, as described above (e.g., a valine encoded by rs734784, a valine encoded by rs1042164, a glutamate encoded by rs749670, a threonine encoded by rs955592 and a glycine encoded by rs1040461).

[0064] Also, target polypeptides may exist as chimeric or fusion polypeptides. As used herein, a target “chimeric polypeptide” or target “fusion polypeptide” includes a target polypeptide linked to a non-target polypeptide. A “non-target polypeptide” refers to a polypeptide having an amino acid sequence corresponding to a polypeptide which is not substantially identical to the target polypeptide, which includes, for example, a polypeptide that is different from the target polypeptide and derived from the same or a different organism. The target polypeptide in the fusion polypeptide can correspond to an entire or nearly entire target polypeptide or a fragment thereof. The non-target polypeptide can be fused to the N-terminus or C-terminus of the target polypeptide.

[0065] Fusion polypeptides can include a moiety having high affinity for a ligand. For example, the fusion polypeptide can be a GST-target fusion polypeptide in which the target sequences are fused to the C-terminus of the GST sequences, or a polyhistidine-target fusion polypeptide in which the target polypeptide is fused at the N- or C-terminus to a string of histidine residues. Such fusion polypeptides can facilitate purification of recombinant target polypeptide. Expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide), and a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A, or a substantially identical nucleotide sequence thereof, can be cloned into an expression vector such that the fusion moiety is linked in-frame to the target polypeptide. Further, the fusion polypeptide can be a target polypeptide containing a heterologous signal sequence at its N-terminus. In certain host cells (e.g., mammalian host cells), expression, secretion, cellular internalization, and cellular localization of a target polypeptide can be increased through use of a heterologous signal sequence. Fusion polypeptides can also include all or a part of a serum polypeptide (e.g., an IgG constant region or human serum albumin).

[0066] Target polypeptides can be incorporated into pharmaceutical compositions and administered to a subject *in vivo*. Administration of these target polypeptides can be used to affect the bioavailability of a substrate of the target polypeptide and may effectively increase target polypeptide biological activity in a cell. Target fusion polypeptides may be useful therapeutically for the treatment of disorders caused by, for example, (i) aberrant modification or mutation of a gene encoding a target polypeptide; (ii) mis-

regulation of the gene encoding the target polypeptide; and (iii) aberrant post-translational modification of a target polypeptide. Also, target polypeptides can be used as immunogens to produce anti-target antibodies in a subject, to purify target polypeptide ligands or binding partners, and in screening assays to identify molecules which inhibit or enhance the interaction of a target polypeptide with a substrate.

[0067] In addition, polypeptides can be chemically synthesized using techniques known in the art (See, *e.g.*, Creighton, 1983 Proteins. New York, N.Y.: W. H. Freeman and Company; and Hunkapiller et al., (1984) Nature July 12 -18;310(5973):105-11). For example, a relative short fragment can be synthesized by use of a peptide synthesizer. Furthermore, if desired, non-classical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the fragment sequence. Non-classical amino acids include, but are not limited to, to the D-isomers of the common amino acids, 2,4-diaminobutyric acid, α -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, γ -Abu, ϵ -Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, fluoroamino acids, designer amino acids such as β -methyl amino acids, Ca-methyl amino acids, Na-methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

[0068] Polypeptides and polypeptide fragments sometimes are differentially modified during or after translation, *e.g.*, by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH₄; acetylation, formylation, oxidation, reduction; metabolic synthesis in the presence of tunicamycin; and the like. Additional post-translational modifications include, for example, N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of prokaryotic host cell expression. The polypeptide fragments may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and isolation of the polypeptide.

[0069] Also provided are chemically modified derivatives of polypeptides that can provide additional advantages such as increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (*see e.g.*, U.S. Pat. No: 4,179,337. The chemical moieties for derivitization may be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and the like. The polypeptides may be modified at random positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

[0070] The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the preferred molecular weight is between about 1 kDa and about 100 kDa (the term “about” indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight) for ease in handling and manufacturing. Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release desired, the effects, if any on biological activity, the ease in handling, the degree or lack of antigenicity and other known effects of the polyethylene glycol to a therapeutic protein or analog).

[0071] The polymers should be attached to the polypeptide with consideration of effects on functional or antigenic domains of the polypeptide. There are a number of attachment methods available to those skilled in the art (*e.g.*, EP 0 401 384 (coupling PEG to G-CSF) and Malik et al. (1992) *Exp Hematol.* September;20(8):1028-35 (pegylation of GM-CSF using tresyl chloride)). For example, polyethylene glycol may be covalently bound through amino acid residues via a reactive group, such as a free amino or carboxyl group. Reactive groups are those to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine residues and the N-terminal amino acid residues; those having a free carboxyl group may include aspartic acid residues, glutamic acid residues and the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group for attaching the polyethylene glycol molecules. For therapeutic purposes, the attachment sometimes is at an amino group, such as attachment at the N-terminus or lysine group.

[0072] Proteins can be chemically modified at the N-terminus. Using polyethylene glycol as an illustration of such a composition, one may select from a variety of polyethylene glycol molecules (by molecular weight, branching, and the like), the proportion of polyethylene glycol molecules to protein (polypeptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (*i.e.*, separating this moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules. Selective proteins chemically modified at the N-terminus may be accomplished by reductive alkylation, which exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivatization in a particular protein. Under the appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus with a carbonyl group containing polymer is achieved.

Substantially Identical Nucleic Acids and Polypeptides

[0073] Nucleotide sequences and polypeptide sequences that are substantially identical to a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A and the target polypeptide sequences encoded by those nucleotide sequences, respectively, are included

herein. The term “substantially identical” as used herein refers to two or more nucleic acids or polypeptides sharing one or more identical nucleotide sequences or polypeptide sequences, respectively. Included are nucleotide sequences or polypeptide sequences that are 55% or more, 60% or more, 65% or more, 70% or more, 75% or more, 80% or more, 85% or more, 90% or more, 95% or more (each often within a 1%, 2%, 3% or 4% variability) identical to a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence, or other nucleotide sequence referenced in Table A, or the encoded target polypeptide amino acid sequences. One test for determining whether two nucleic acids are substantially identical is to determine the percent of identical nucleotide sequences or polypeptide sequences shared between the nucleic acids or polypeptides.

[0074] Calculations of sequence identity are often performed as follows. Sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). The length of a reference sequence aligned for comparison purposes is sometimes 30% or more, 40% or more, 50% or more, often 60% or more, and more often 70% or more, 80% or more, 90% or more, or 100% of the length of the reference sequence. The nucleotides or amino acids at corresponding nucleotide or polypeptide positions, respectively, are then compared among the two sequences. When a position in the first sequence is occupied by the same nucleotide or amino acid as the corresponding position in the second sequence, the nucleotides or amino acids are deemed to be identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, introduced for optimal alignment of the two sequences.

[0075] Comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. Percent identity between two amino acid or nucleotide sequences can be determined using the algorithm of Meyers & Miller, *CABIOS 4*: 11-17 (1989), which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. Also, percent identity between two amino acid sequences can be determined using the Needleman & Wunsch, *J. Mol. Biol.* 48: 444-453 (1970) algorithm which has been incorporated into the GAP program in the GCG software package (available at the http address www.gcg.com), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. Percent identity between two nucleotide sequences can be determined using the GAP program in the GCG software package (available at http address www.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A set of parameters often used is a Blossum 62 scoring matrix with a gap open penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

[0076] Another manner for determining if two nucleic acids are substantially identical is to assess whether a polynucleotide homologous to one nucleic acid will hybridize to the other nucleic acid under stringent conditions. As use herein, the term “stringent conditions” refers to conditions for hybridization and washing. Stringent conditions are known to those skilled in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. , 6.3.1-6.3.6 (1989). Aqueous and non-aqueous methods are described in that reference and either can be used. An example of stringent hybridization conditions is hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50°C. Another example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 55°C. A further example of stringent hybridization conditions is hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 60°C. Often, stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 65°C. More often, stringency conditions are 0.5M sodium phosphate, 7% SDS at 65°C, followed by one or more washes at 0.2X SSC, 1% SDS at 65°C.

[0077] An example of a substantially identical nucleotide sequence to a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A is one that has a different nucleotide sequence but still encodes the same polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A. Another example is a nucleotide sequence that encodes a polypeptide having a polypeptide sequence that is more than 70% or more identical to, sometimes more than 75% or more, 80% or more, or 85% or more identical to, and often more than 90% or more and 95% or more identical to a polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A.

[0078] Nucleotide sequences in SEQ ID NO: 1-3 or referenced in Table A and amino acid sequences of encoded polypeptides can be used as “query sequences” to perform a search against public databases to identify other family members or related sequences, for example. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul *et al.*, *J. Mol. Biol.* 215: 403-10 (1990). BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to nucleotide sequences in SEQ ID NO: 1-3 or referenced in Table A. BLAST polypeptide searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to polypeptides encoded by the nucleotide sequences of SEQ ID NO: 1-3 or referenced in Table A. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, *Nucleic Acids Res.* 25(17): 3389-3402 (1997). When utilizing BLAST and Gapped BLAST programs, default parameters of

the respective programs (*e.g.*, XBLAST and NBLAST) can be used (*see* the http address www.ncbi.nlm.nih.gov).

[0079] A nucleic acid that is substantially identical to a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A may include polymorphic sites at positions equivalent to those described herein when the sequences are aligned. For example, using the alignment procedures described herein, SNPs in a sequence substantially identical to a sequence in SEQ ID NO: 1-3 or referenced in Table A can be identified at nucleotide positions that match (*i.e.*, align) with nucleotides at SNP positions in each nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A. Also, where a polymorphic variation results in an insertion or deletion, insertion or deletion of a nucleotide sequence from a reference sequence can change the relative positions of other polymorphic sites in the nucleotide sequence.

[0080] Substantially identical nucleotide and polypeptide sequences include those that are naturally occurring, such as allelic variants (same locus), splice variants, homologs (different locus), and orthologs (different organism) or can be non-naturally occurring. Non-naturally occurring variants can be generated by mutagenesis techniques, including those applied to polynucleotides, cells, or organisms. The variants can contain nucleotide substitutions, deletions, inversions and insertions. Variation can occur in either or both the coding and non-coding regions. The variations can produce both conservative and non-conservative amino acid substitutions (as compared in the encoded product). Orthologs, homologs, allelic variants, and splice variants can be identified using methods known in the art. These variants normally comprise a nucleotide sequence encoding a polypeptide that is 50% or more, about 55% or more, often about 70-75% or more or about 80-85% or more, and sometimes about 90-95% or more identical to the amino acid sequences of target polypeptides or a fragment thereof. Such nucleic acid molecules can readily be identified as being able to hybridize under stringent conditions to a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A or a fragment of this sequence. Nucleic acid molecules corresponding to orthologs, homologs, and allelic variants of a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A can further be identified by mapping the sequence to the same chromosome or locus as the nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A.

[0081] Also, substantially identical nucleotide sequences may include codons that are altered with respect to the naturally occurring sequence for enhancing expression of a target polypeptide in a particular expression system. For example, the nucleic acid can be one in which one or more codons are altered, and often 10% or more or 20% or more of the codons are altered for optimized expression in bacteria (*e.g.*, *E. coli*), yeast (*e.g.*, *S. cerevisiae*), human (*e.g.*, 293 cells), insect, or rodent (*e.g.*, hamster) cells.

Methods for Identifying Risk of Osteoarthritis

[0082] Methods for prognosing and diagnosing osteoarthritis are included herein. These methods include detecting the presence or absence of one or more polymorphic variations in a nucleotide sequence associated with osteoarthritis, such as variants in or around the loci set forth herein, or a substantially identical sequence thereof, in a sample from a subject, where the presence of a polymorphic variant described herein is indicative of a risk of osteoarthritis. Determining a risk of osteoarthritis sometimes refers to determining whether an individual is at an increased risk of osteoarthritis (e.g., intermediate risk or higher risk).

[0083] Thus, featured herein is a method for identifying a subject who is at risk of osteoarthritis, which comprises detecting an aberration associated with osteoarthritis in a nucleic acid sample from the subject. An embodiment is a method for detecting a risk of osteoarthritis in a subject, which comprises detecting the presence or absence of a polymorphic variation associated with osteoarthritis at a polymorphic site in a nucleotide sequence in a nucleic acid sample from a subject, where the nucleotide sequence comprises a polynucleotide sequence selected from the group consisting of: (a) a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A; (b) a nucleotide sequence which encodes a polypeptide consisting of an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A; (c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A, or a nucleotide sequence about 90% or more identical to a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A; and (d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising the polymorphic site; whereby the presence of the polymorphic variation is indicative of a predisposition to osteoarthritis in the subject. In certain embodiments, polymorphic variants at the positions described herein are detected for determining a risk of osteoarthritis, and polymorphic variants at positions in linkage disequilibrium with these positions are detected for determining a risk of osteoarthritis. As used herein, the terms "SEQ ID NO: 1-3" and other nucleotide sequences "referenced in Table A" refers to individual sequences in SEQ ID NO: 1, 2 or 3 or any individual sequence referenced in Table A, each sequence being separately applicable to embodiments described herein.

[0084] Risk of osteoarthritis sometimes is expressed as a probability, such as an odds ratio, percentage, or risk factor. Risk often is based upon the presence or absence of one or more polymorphic variants described herein, and also may be based in part upon phenotypic traits of the individual being tested. Methods for calculating risk based upon patient data are well known (*see, e.g., Agresti, Categorical Data Analysis*, 2nd Ed. 2002. Wiley). Allelotyping and genotyping analyses may be carried out in populations other than those exemplified herein to enhance the predictive power of the prognostic method. These further analyses are executed in view of the exemplified procedures described herein, and may be based upon the same polymorphic variations or additional polymorphic variations.

[0085] In certain embodiments, determining the presence of a combination of two or more polymorphic variants associated with osteoarthritis in one or more genetic loci (e.g., one or more genes) of the sample is determined to identify, quantify and/or estimate, risk of osteoarthritis. The risk often is the probability of having or developing osteoarthritis. The risk sometimes is expressed as a relative risk with respect to a population average risk of osteoarthritis, and sometimes is expressed as a relative risk with respect to the lowest risk group. Such relative risk assessments often are based upon penetrance values determined by statistical methods, and are particularly useful to clinicians and insurance companies for assessing risk of osteoarthritis (e.g., a clinician can target appropriate detection, prevention and therapeutic regimens to a patient after determining the patient's risk of osteoarthritis, and an insurance company can fine tune actuarial tables based upon population genotype assessments of osteoarthritis risk). Risk of osteoarthritis sometimes is expressed as an odds ratio, which is the odds of a particular person having a genotype has or will develop osteoarthritis with respect to another genotype group (e.g., the most disease protective genotype or population average). In related embodiments, the determination is utilized to identify a subject at risk of osteoarthritis. In an embodiment, two or more polymorphic variations are detected in two or more regions in human genomic DNA associated with increased risk of osteoarthritis, such as a locus containing a *KIAA0296*, *chrom 4* or *SNW1* or other locus referenced in Table A, for example. In certain embodiments, 3 or more, or 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 or more polymorphic variants are detected in the sample. In specific embodiments, polymorphic variants are detected in a *KIAA0296*, *chrom 4* or *SNW1* region or other region referenced in Table A, for example. In another embodiment, polymorphic variants are detected at two or three positions in a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A. In certain embodiments, polymorphic variants are detected at other genetic loci (e.g., the polymorphic variants can be detected in a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A in addition to other loci or only in other loci), where the other loci include but are not limited to those described in concurrently-filed patent applications having attorney docket number 524593008700, 524593008800, 524593008900, 524593009000, 524593009100 or 524593009200, each of which is incorporated herein by reference in its entirety.

[0086] Results from prognostic tests may be combined with other test results to diagnose osteoarthritis. For example, prognostic results may be gathered, a patient sample may be ordered based on a determined predisposition to osteoarthritis, the patient sample is analyzed, and the results of the analysis may be utilized to diagnose osteoarthritis. Also osteoarthritis diagnostic method can be developed from studies used to generate prognostic methods in which populations are stratified into subpopulations having different progressions of osteoarthritis. In another embodiment, prognostic results may be gathered, a patient's risk factors for developing osteoarthritis (e.g., age, weight, race, diet) analyzed, and a patient sample may be ordered based on a determined predisposition to osteoarthritis.

[0087] The nucleic acid sample typically is isolated from a biological sample obtained from a subject. For example, nucleic acid can be isolated from blood, saliva, sputum, urine, cell scrapings, and biopsy tissue. The nucleic acid sample can be isolated from a biological sample using standard techniques, such as the technique described in Example 2. As used herein, the term “subject” refers primarily to humans but also refers to other mammals such as dogs, cats, and ungulates (*e.g.*, cattle, sheep, and swine). Subjects also include avians (*e.g.*, chickens and turkeys), reptiles, and fish (*e.g.*, salmon), as embodiments described herein can be adapted to nucleic acid samples isolated from any of these organisms. The nucleic acid sample may be isolated from the subject and then directly utilized in a method for determining the presence of a polymorphic variant, or alternatively, the sample may be isolated and then stored (*e.g.*, frozen) for a period of time before being subjected to analysis.

[0088] The presence or absence of a polymorphic variant is determined using one or both chromosomal complements represented in the nucleic acid sample. Determining the presence or absence of a polymorphic variant in both chromosomal complements represented in a nucleic acid sample from a subject having a copy of each chromosome is useful for determining the zygosity of an individual for the polymorphic variant (*i.e.*, whether the individual is homozygous or heterozygous for the polymorphic variant). Any oligonucleotide-based diagnostic may be utilized to determine whether a sample includes the presence or absence of a polymorphic variant in a sample. For example, primer extension methods, ligase sequence determination methods (*e.g.*, U.S. Pat. Nos. 5,679,524 and 5,952,174, and WO 01/27326), mismatch sequence determination methods (*e.g.*, U.S. Pat. Nos. 5,851,770; 5,958,692; 6,110,684; and 6,183,958), microarray sequence determination methods, restriction fragment length polymorphism (RFLP), single strand conformation polymorphism detection (SSCP) (*e.g.*, U.S. Pat. Nos. 5,891,625 and 6,013,499), PCR-based assays (*e.g.*, TAQMAN[®] PCR System (Applied Biosystems)), and nucleotide sequencing methods may be used.

[0089] Oligonucleotide extension methods typically involve providing a pair of oligonucleotide primers in a polymerase chain reaction (PCR) or in other nucleic acid amplification methods for the purpose of amplifying a region from the nucleic acid sample that comprises the polymorphic variation. One oligonucleotide primer is complementary to a region 3' of the polymorphism and the other is complementary to a region 5' of the polymorphism. A PCR primer pair may be used in methods disclosed in U.S. Pat. Nos. 4,683,195; 4,683,202, 4,965,188; 5,656,493; 5,998,143; 6,140,054; WO 01/27327; and WO 01/27329 for example. PCR primer pairs may also be used in any commercially available machines that perform PCR, such as any of the GENEAMP[®] Systems available from Applied Biosystems. Also, those of ordinary skill in the art will be able to design oligonucleotide primers based upon a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A using knowledge available in the art.

[0090] Also provided is an extension oligonucleotide that hybridizes to the amplified fragment adjacent to the polymorphic variation. As used herein, the term “adjacent” refers to the 3’ end of the extension oligonucleotide being often 1 nucleotide from the 5’ end of the polymorphic site, and sometimes 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides from the 5’ end of the polymorphic site, in the nucleic acid when the extension oligonucleotide is hybridized to the nucleic acid. The extension oligonucleotide then is extended by one or more nucleotides, and the number and/or type of nucleotides that are added to the extension oligonucleotide determine whether the polymorphic variant is present. Oligonucleotide extension methods are disclosed, for example, in U.S. Pat. Nos. 4,656,127; 4,851,331; 5,679,524; 5,834,189; 5,876,934; 5,908,755; 5,912,118; 5,976,802; 5,981,186; 6,004,744; 6,013,431; 6,017,702; 6,046,005; 6,087,095; 6,210,891; and WO 01/20039. Oligonucleotide extension methods using mass spectrometry are described, for example, in U.S. Pat. Nos. 5,547,835; 5,605,798; 5,691,141; 5,849,542; 5,869,242; 5,928,906; 6,043,031; and 6,194,144, and a method often utilized is described herein in Example 2.

[0091] A microarray can be utilized for determining whether a polymorphic variant is present or absent in a nucleic acid sample. A microarray may include any oligonucleotides described herein, and methods for making and using oligonucleotide microarrays suitable for diagnostic use are disclosed in U.S. Pat. Nos. 5,492,806; 5,525,464; 5,589,330; 5,695,940; 5,849,483; 6,018,041; 6,045,996; 6,136,541; 6,142,681; 6,156,501; 6,197,506; 6,223,127; 6,225,625; 6,229,911; 6,239,273; WO 00/52625; WO 01/25485; and WO 01/29259. The microarray typically comprises a solid support and the oligonucleotides may be linked to this solid support by covalent bonds or by non-covalent interactions. The oligonucleotides may also be linked to the solid support directly or by a spacer molecule. A microarray may comprise one or more oligonucleotides complementary to a polymorphic site set forth herein.

[0092] A kit also may be utilized for determining whether a polymorphic variant is present or absent in a nucleic acid sample. A kit often comprises one or more pairs of oligonucleotide primers useful for amplifying a fragment of a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A or a substantially identical sequence thereof, where the fragment includes a polymorphic site. The kit sometimes comprises a polymerizing agent, for example, a thermostable nucleic acid polymerase such as one disclosed in U.S. Pat. Nos. 4,889,818 or 6,077,664. Also, the kit often comprises an elongation oligonucleotide that hybridizes to a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A in a nucleic acid sample adjacent to the polymorphic site. Where the kit includes an elongation oligonucleotide, it also often comprises chain elongating nucleotides, such as dATP, dTTP, dGTP, dCTP, and dITP, including analogs of dATP, dTTP, dGTP, dCTP and dITP, provided that such analogs are substrates for a thermostable nucleic acid polymerase and can be incorporated into a nucleic acid chain elongated from the extension oligonucleotide. Along with chain

elongating nucleotides would be one or more chain terminating nucleotides such as ddATP, ddTTP, ddGTP, ddCTP, and the like. In an embodiment, the kit comprises one or more oligonucleotide primer pairs, a polymerizing agent, chain elongating nucleotides, at least one elongation oligonucleotide, and one or more chain terminating nucleotides. Kits optionally include buffers, vials, microtiter plates, and instructions for use.

[0093] An individual identified as being at risk of osteoarthritis may be heterozygous or homozygous with respect to the allele associated with a higher risk of osteoarthritis. A subject homozygous for an allele associated with an increased risk of osteoarthritis is at a comparatively high risk of osteoarthritis, a subject heterozygous for an allele associated with an increased risk of osteoarthritis is at a comparatively intermediate risk of osteoarthritis, and a subject homozygous for an allele associated with a decreased risk of osteoarthritis is at a comparatively low risk of osteoarthritis. A genotype may be assessed for a complementary strand, such that the complementary nucleotide at a particular position is detected.

[0094] Also featured are methods for determining risk of osteoarthritis and/or identifying a subject at risk of osteoarthritis by contacting a polypeptide or protein encoded by a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A from a subject with an antibody that specifically binds to an epitope associated with increased risk of osteoarthritis in the polypeptide.

Applications of Prognostic and Diagnostic Results to Pharmacogenomic Methods

[0095] Pharmacogenomics is a discipline that involves tailoring a treatment for a subject according to the subject's genotype as a particular treatment regimen may exert a differential effect depending upon the subject's genotype. For example, based upon the outcome of a prognostic test described herein, a clinician or physician may target pertinent information and preventative or therapeutic treatments to a subject who would be benefited by the information or treatment and avoid directing such information and treatments to a subject who would not be benefited (*e.g.*, the treatment has no therapeutic effect and/or the subject experiences adverse side effects).

[0096] The following is an example of a pharmacogenomic embodiment. A particular treatment regimen can exert a differential effect depending upon the subject's genotype. Where a candidate therapeutic exhibits a significant interaction with a major allele and a comparatively weak interaction with a minor allele (*e.g.*, an order of magnitude or greater difference in the interaction), such a therapeutic typically would not be administered to a subject genotyped as being homozygous for the minor allele, and sometimes not administered to a subject genotyped as being heterozygous for the minor allele. In another example, where a candidate therapeutic is not significantly toxic when administered to subjects who are homozygous for a major allele but is comparatively toxic when administered to subjects

heterozygous or homozygous for a minor allele, the candidate therapeutic is not typically administered to subjects who are genotyped as being heterozygous or homozygous with respect to the minor allele.

[0097] The methods described herein are applicable to pharmacogenomic methods for preventing, alleviating or treating osteoarthritis. For example, a nucleic acid sample from an individual may be subjected to a prognostic test described herein. Where one or more polymorphic variations associated with increased risk of osteoarthritis are identified in a subject, information for preventing or treating osteoarthritis and/or one or more osteoarthritis treatment regimens then may be prescribed to that subject.

[0098] In certain embodiments, a treatment or preventative regimen is specifically prescribed and/or administered to individuals who will most benefit from it based upon their risk of developing osteoarthritis assessed by the methods described herein. Thus, provided are methods for identifying a subject predisposed to osteoarthritis and then prescribing a therapeutic or preventative regimen to individuals identified as having a predisposition. Thus, certain embodiments are directed to a method for reducing osteoarthritis in a subject, which comprises: detecting the presence or absence of a polymorphic variant associated with osteoarthritis in a nucleotide sequence in a nucleic acid sample from a subject, where the nucleotide sequence comprises a polynucleotide sequence selected from the group consisting of: (a) a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A; (b) a nucleotide sequence which encodes a polypeptide consisting of an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A; (c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A, or a nucleotide sequence about 90% or more identical to a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A; and (d) a fragment of a polynucleotide sequence of (a), (b), or (c); and prescribing or administering a treatment regimen to a subject from whom the sample originated where the presence of a polymorphic variation associated with osteoarthritis is detected in the nucleotide sequence. In these methods, predisposition results may be utilized in combination with other test results to diagnose osteoarthritis.

[0099] Certain preventative treatments often are prescribed to subjects having a predisposition to osteoarthritis and where the subject is diagnosed with osteoarthritis or is diagnosed as having symptoms indicative of an early stage of osteoarthritis. The treatment sometimes is preventative (*e.g.*, is prescribed or administered to reduce the probability that osteoarthritis arises or progresses), sometimes is therapeutic, and sometimes delays, alleviates or halts the progression of osteoarthritis. Any known preventative or therapeutic treatment for alleviating or preventing the occurrence of osteoarthritis is prescribed and/or administered. For example, the treatment often is directed to decreasing pain and improving joint movement. Examples of OA treatments include exercises to keep joints flexible and improve muscle strength. Different medications to control pain, including corticosteroids and nonsteroidal anti-inflammatory drugs (NSAIDs, *e.g.*, Voltaren); cyclooxygenase-2 (COX-2) inhibitors

(e.g., Celebrex, Vioxx, Mobic, and Bextra); monoclonal antibodies (e.g., Remicade); tumor necrosis factor inhibitors (e.g., Enbrel); or injections of glucocorticoids, hyaluronic acid or chondroitin sulfate into joints that are inflamed and not responsive to NSAIDs. Orally administered chondroitin sulfate also may be used as a therapeutic, as it may increase hyaluronic acid levels and viscosity of synovial fluid, and decrease collagenase levels in synovial fluid. Also, glucosamine can serve as an OA therapeutic as delivering it into joints may inhibit enzymes involved in cartilage degradation and enhance the production of hyaluronic acid. For mild pain without inflammation, acetaminophen may be used. Other treatments include: heat/cold therapy for temporary pain relief; joint protection to prevent strain or stress on painful joints; surgery to relieve chronic pain in damaged joints; and weight control to prevent extra stress on weight-bearing joints.

[0100] As therapeutic approaches for treating osteoarthritis continue to evolve and improve, the goal of treatments for osteoarthritis related disorders is to intervene even before clinical signs first manifest. Thus, genetic markers associated with susceptibility to osteoarthritis prove useful for early diagnosis, prevention and treatment of osteoarthritis.

[0101] As osteoarthritis preventative and treatment information can be specifically targeted to subjects in need thereof (e.g., those at risk of developing osteoarthritis or those in an early stage of osteoarthritis), provided herein is a method for preventing or reducing the risk of developing osteoarthritis in a subject, which comprises: (a) detecting the presence or absence of a polymorphic variation associated with osteoarthritis at a polymorphic site in a nucleotide sequence in a nucleic acid sample from a subject; (b) identifying a subject with a predisposition to osteoarthritis, whereby the presence of the polymorphic variation is indicative of a predisposition to osteoarthritis in the subject; and (c) if such a predisposition is identified, providing the subject with information about methods or products to prevent or reduce osteoarthritis or to delay the onset of osteoarthritis. Also provided is a method of targeting information or advertising to a subpopulation of a human population based on the subpopulation being genetically predisposed to a disease or condition, which comprises: (a) detecting the presence or absence of a polymorphic variation associated with osteoarthritis at a polymorphic site in a nucleotide sequence in a nucleic acid sample from a subject; (b) identifying the subpopulation of subjects in which the polymorphic variation is associated with osteoarthritis; and (c) providing information only to the subpopulation of subjects about a particular product which may be obtained and consumed or applied by the subject to help prevent or delay onset of the disease or condition.

[0102] Pharmacogenomics methods also may be used to analyze and predict a response to osteoarthritis treatment or a drug. For example, if pharmacogenomics analysis indicates a likelihood that an individual will respond positively to osteoarthritis treatment with a particular drug, the drug may be administered to the individual. Conversely, if the analysis indicates that an individual is likely to respond negatively to treatment with a particular drug, an alternative course of treatment may be prescribed. A

negative response may be defined as either the absence of an efficacious response or the presence of toxic side effects. The response to a therapeutic treatment can be predicted in a background study in which subjects in any of the following populations are genotyped: a population that responds favorably to a treatment regimen, a population that does not respond significantly to a treatment regimen, and a population that responds adversely to a treatment regimen (*e.g.*, exhibits one or more side effects). These populations are provided as examples and other populations and subpopulations may be analyzed. Based upon the results of these analyses, a subject is genotyped to predict whether he or she will respond favorably to a treatment regimen, not respond significantly to a treatment regimen, or respond adversely to a treatment regimen.

[0103] The tests described herein also are applicable to clinical drug trials. One or more polymorphic variants indicative of response to an agent for treating osteoarthritis or to side effects to an agent for treating osteoarthritis may be identified using the methods described herein. Thereafter, potential participants in clinical trials of such an agent may be screened to identify those individuals most likely to respond favorably to the drug and exclude those likely to experience side effects. In that way, the effectiveness of drug treatment may be measured in individuals who respond positively to the drug, without lowering the measurement as a result of the inclusion of individuals who are unlikely to respond positively in the study and without risking undesirable safety problems.

[0104] Thus, another embodiment is a method of selecting an individual for inclusion in a clinical trial of a treatment or drug comprising the steps of: (a) obtaining a nucleic acid sample from an individual; (b) determining the identity of a polymorphic variation which is associated with a positive response to the treatment or the drug, or at least one polymorphic variation which is associated with a negative response to the treatment or the drug in the nucleic acid sample, and (c) including the individual in the clinical trial if the nucleic acid sample contains said polymorphic variation associated with a positive response to the treatment or the drug or if the nucleic acid sample lacks said polymorphic variation associated with a negative response to the treatment or the drug. In addition, the methods described herein for selecting an individual for inclusion in a clinical trial of a treatment or drug encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination. The polymorphic variation may be in a sequence selected individually or in any combination from the group consisting of (i) a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A; (ii) a nucleotide sequence which encodes a polypeptide consisting of an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A; (iii) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to an amino acid sequence encoded by a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A, or a nucleotide sequence about 90% or more identical to a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A; and (iv) a fragment of a polynucleotide sequence of (i), (ii), or (iii) comprising the polymorphic site. The including

step (c) optionally comprises administering the drug or the treatment to the individual if the nucleic acid sample contains the polymorphic variation associated with a positive response to the treatment or the drug and the nucleic acid sample lacks said biallelic marker associated with a negative response to the treatment or the drug.

[0105] Also provided herein is a method of partnering between a diagnostic/prognostic testing provider and a provider of a consumable product, which comprises: (a) the diagnostic/prognostic testing provider detects the presence or absence of a polymorphic variation associated with osteoarthritis at a polymorphic site in a nucleotide sequence in a nucleic acid sample from a subject; (b) the diagnostic/prognostic testing provider identifies the subpopulation of subjects in which the polymorphic variation is associated with osteoarthritis; (c) the diagnostic/prognostic testing provider forwards information to the subpopulation of subjects about a particular product which may be obtained and consumed or applied by the subject to help prevent or delay onset of the disease or condition; and (d) the provider of a consumable product forwards to the diagnostic test provider a fee every time the diagnostic/prognostic test provider forwards information to the subject as set forth in step (c) above.

Compositions Comprising Osteoarthritis-Directed Molecules

[0106] Featured herein is a composition comprising a cell from a subject having osteoarthritis or at risk of osteoarthritis and one or more molecules specifically directed and targeted to a nucleic acid comprising a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence, other nucleotide sequence referenced in Table A, or an encoded amino acid sequence. Such directed molecules include, but are not limited to, a compound that binds to a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence, or other nucleotide sequence referenced in Table A, or encoded amino acid sequence; a RNAi or siRNA molecule having a strand complementary or substantially complementary to a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A (e.g., hybridizes to a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A under conditions of high stringency); an antisense nucleic acid complementary or substantially complementary to an RNA encoded by a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A (e.g., hybridizes to a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A under conditions of high stringency); a ribozyme that hybridizes to a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A (e.g., hybridizes to a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A under conditions of high stringency); a nucleic acid aptamer that specifically binds a polypeptide encoded by a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A; and an antibody that specifically binds to a polypeptide encoded by a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A or

binds to a nucleic acid having such a nucleotide sequence. In an embodiment, the antibody selectively binds to an epitope comprising an amino acid encoded by rs734784, rs1042164, rs749670, rs955592 and rs1040461. In specific embodiments, the osteoarthritis directed molecule interacts with a nucleic acid or polypeptide variant associated with osteoarthritis, such as variants referenced herein. In other embodiments, the osteoarthritis directed molecule interacts with a polypeptide involved in a signal pathway of a polypeptide encoded by a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A, or a nucleic acid comprising such a nucleotide sequence.

[0107] Compositions sometimes include an adjuvant known to stimulate an immune response, and in certain embodiments, an adjuvant that stimulates a T-cell lymphocyte response. Adjuvants are known, including but not limited to an aluminum adjuvant (e.g., aluminum hydroxide); a cytokine adjuvant or adjuvant that stimulates a cytokine response (e.g., interleukin (IL)-12 and/or gamma-interferon cytokines); a Freund-type mineral oil adjuvant emulsion (e.g., Freund's complete or incomplete adjuvant); a synthetic lipid compound; a copolymer adjuvant (e.g., TitreMax); a saponin; Quil A; a liposome; an oil-in-water emulsion (e.g., an emulsion stabilized by Tween 80 and pluronic polyoxyethylene/polyoxypropylene block copolymer (Syntex Adjuvant Formulation); TitreMax; detoxified endotoxin (MPL) and mycobacterial cell wall components (TDW, CWS) in 2% squalene (Ribi Adjuvant System)); a muramyl dipeptide; an immune-stimulating complex (ISCOM, e.g., an Ag-modified saponin/cholesterol micelle that forms stable cage-like structure); an aqueous phase adjuvant that does not have a depot effect (e.g., Gerbu adjuvant); a carbohydrate polymer (e.g., AdjuPrime); L-tyrosine; a manide-oleate compound (e.g., Montanide); an ethylene-vinyl acetate copolymer (e.g., Elvax 40W1,2); or lipid A, for example. Such compositions are useful for generating an immune response against osteoarthritis directed molecule (e.g., an HLA-binding subsequence within a polypeptide encoded by a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence). In such methods, a peptide having an amino acid subsequence of a polypeptide encoded by a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence is delivered to a subject, where the subsequence binds to an HLA molecule and induces a CTL lymphocyte response. The peptide sometimes is delivered to the subject as an isolated peptide or as a minigene in a plasmid that encodes the peptide. Methods for identifying HLA-binding subsequences in such polypeptides are known (see e.g., publication WO02/20616 and PCT application US98/01373 for methods of identifying such sequences).

[0108] The cell may be in a group of cells cultured *in vitro* or in a tissue maintained *in vitro* or present in an animal *in vivo* (e.g., a rat, mouse, ape or human). In certain embodiments, a composition comprises a component from a cell such as a nucleic acid molecule (e.g., genomic DNA), a protein mixture or isolated protein, for example. The aforementioned compositions have utility in diagnostic, prognostic and pharmacogenomic methods described previously and in therapeutics described hereafter. Certain osteoarthritis directed molecules are described in greater detail below.

Compounds

[0109] Compounds can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; peptoid libraries (libraries of molecules having the functionalities of peptides, but with a novel, non-peptide backbone which are resistant to enzymatic degradation but which nevertheless remain bioactive (see, e.g., Zuckermann et al., J. Med. Chem. 37: 2678-85 (1994)); spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; "one-bead one-compound" library methods; and synthetic library methods using affinity chromatography selection. Biological library and peptoid library approaches are typically limited to peptide libraries, while the other approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, Anticancer Drug Des. 12: 145, (1997)). Examples of methods for synthesizing molecular libraries are described, for example, in DeWitt et al., Proc. Natl. Acad. Sci. U.S.A. 90: 6909 (1993); Erb et al., Proc. Natl. Acad. Sci. USA 91: 11422 (1994); Zuckermann et al., J. Med. Chem. 37: 2678 (1994); Cho et al., Science 261: 1303 (1993); Carrell et al., Angew. Chem. Int. Ed. Engl. 33: 2059 (1994); Carell et al., Angew. Chem. Int. Ed. Engl. 33: 2061 (1994); and in Gallop et al., J. Med. Chem. 37: 1233 (1994).

[0110] Libraries of compounds may be presented in solution (e.g., Houghten, Biotechniques 13: 412-421 (1992)), or on beads (Lam, Nature 354: 82-84 (1991)), chips (Fodor, Nature 364: 555-556 (1993)), bacteria or spores (Ladner, United States Patent No. 5,223,409), plasmids (Cull et al., Proc. Natl. Acad. Sci. USA 89: 1865-1869 (1992)) or on phage (Scott and Smith, Science 249: 386-390 (1990); Devlin, Science 249: 404-406 (1990); Cwirla et al., Proc. Natl. Acad. Sci. 87: 6378-6382 (1990); Felici, J. Mol. Biol. 222: 301-310 (1991); Ladner supra.).

[0111] A compound sometimes alters expression and sometimes alters activity of a polypeptide target and may be a small molecule. Small molecules include, but are not limited to, peptides, peptidomimetics (e.g., peptoids), amino acids, amino acid analogs, polynucleotides, polynucleotide analogs, nucleotides, nucleotide analogs, organic or inorganic compounds (i.e., including heteroorganic and organometallic compounds) having a molecular weight less than about 10,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 5,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 1,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 500 grams per mole, and salts, esters, and other pharmaceutically acceptable forms of such compounds.

Antisense Nucleic Acid Molecules, Ribozymes, RNAi, siRNA and Modified Nucleic Acid Molecules

[0112] An "antisense" nucleic acid refers to a nucleotide sequence complementary to a "sense" nucleic acid encoding a polypeptide, e.g., complementary to the coding strand of a double-stranded

cDNA molecule or complementary to an mRNA sequence. The antisense nucleic acid can be complementary to an entire coding strand, or to a portion thereof or a substantially identical sequence thereof. In another embodiment, the antisense nucleic acid molecule is antisense to a “noncoding region” of the coding strand of a nucleotide sequence (e.g., 5' and 3' untranslated regions in SEQ ID NO: 1-3 or a nucleotide sequence referenced in Table A).

[0113] An antisense nucleic acid can be designed such that it is complementary to the entire coding region of an mRNA encoded by a nucleotide sequence (e.g., SEQ ID NO: 1-3 or a nucleotide sequence referenced in Table A), and often the antisense nucleic acid is an oligonucleotide antisense to only a portion of a coding or noncoding region of the mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of the mRNA, e.g., between the -10 and +10 regions of the target gene nucleotide sequence of interest. An antisense oligonucleotide can be, for example, about 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, or more nucleotides in length. The antisense nucleic acids, which include the ribozymes described hereafter, can be designed to target a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence, often a variant associated with osteoarthritis, or a substantially identical sequence thereof. Among the variants, minor alleles and major alleles can be targeted, and those associated with a higher risk of osteoarthritis are often designed, tested, and administered to subjects.

[0114] An antisense nucleic acid can be constructed using chemical synthesis and enzymatic ligation reactions using standard procedures. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Antisense nucleic acid also can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

[0115] When utilized as therapeutics, antisense nucleic acids typically are administered to a subject (e.g., by direct injection at a tissue site) or generated in situ such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a polypeptide and thereby inhibit expression of the polypeptide, for example, by inhibiting transcription and/or translation. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then are administered systemically. For systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, for example, by linking antisense nucleic acid molecules to peptides or antibodies which bind to cell surface receptors or antigens. Antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. Sufficient intracellular

concentrations of antisense molecules are achieved by incorporating a strong promoter, such as a pol II or pol III promoter, in the vector construct.

[0116] Antisense nucleic acid molecules sometimes are alpha-anomeric nucleic acid molecules. An alpha-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual beta-units, the strands run parallel to each other (Gaultier et al., *Nucleic Acids. Res.* 15: 6625-6641 (1987)). Antisense nucleic acid molecules can also comprise a 2'-o-methylribonucleotide (Inoue et al., *Nucleic Acids Res.* 15: 6131-6148 (1987)) or a chimeric RNA-DNA analogue (Inoue et al., *FEBS Lett.* 215: 327-330 (1987)). Antisense nucleic acids sometimes are composed of DNA or PNA or any other nucleic acid derivatives described previously.

[0117] In another embodiment, an antisense nucleic acid is a ribozyme. A ribozyme having specificity for a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A can include one or more sequences complementary to such a nucleotide sequence, and a sequence having a known catalytic region responsible for mRNA cleavage (see e.g., U.S. Pat. No. 5,093,246 or Haselhoff and Gerlach, *Nature* 334: 585-591 (1988)). For example, a derivative of a Tetrahymena L-19 IVS RNA is sometimes utilized in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a mRNA (see e.g., Cech et al. U.S. Patent No. 4,987,071; and Cech et al. U.S. Patent No. 5,116,742). Also, target mRNA sequences can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules (see e.g., Bartel & Szostak, *Science* 261: 1411-1418 (1993)).

[0118] Osteoarthritis directed molecules include in certain embodiments nucleic acids that can form triple helix structures with a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A, or a substantially identical sequence thereof, especially one that includes a regulatory region that controls expression of a polypeptide. Gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of a nucleotide sequence referenced herein or a substantially identical sequence (e.g., promoter and/or enhancers) to form triple helical structures that prevent transcription of a gene in target cells (see e.g., Helene, *Anticancer Drug Des.* 6(6): 569-84 (1991); Helene et al., *Ann. N.Y. Acad. Sci.* 660: 27-36 (1992); and Maher, *Bioassays* 14(12): 807-15 (1992). Potential sequences that can be targeted for triple helix formation can be increased by creating a so-called "switchback" nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizeable stretch of either purines or pyrimidines to be present on one strand of a duplex.

[0119] Osteoarthritis directed molecules include RNAi and siRNA nucleic acids. Gene expression may be inhibited by the introduction of double-stranded RNA (dsRNA), which induces potent and specific gene silencing, a phenomenon called RNA interference or RNAi. See, e.g., Fire et al., US Patent

Number 6,506,559; Tuschl et al. PCT International Publication No. WO 01/75164; Kay et al. PCT International Publication No. WO 03/010180A1; or Bosher JM, Labouesse, Nat Cell Biol 2000 Feb;2(2):E31-6. This process has been improved by decreasing the size of the double-stranded RNA to 20-24 base pairs (to create small-interfering RNAs or siRNAs) that “switched off” genes in mammalian cells without initiating an acute phase response, i.e., a host defense mechanism that often results in cell death (see, e.g., Caplen et al. Proc Natl Acad Sci U S A. 2001 Aug 14;98(17):9742-7 and Elbashir et al. Methods 2002 Feb;26(2):199-213). There is increasing evidence of post-transcriptional gene silencing by RNA interference (RNAi) for inhibiting targeted expression in mammalian cells at the mRNA level, in human cells. There is additional evidence of effective methods for inhibiting the proliferation and migration of tumor cells in human patients, and for inhibiting metastatic cancer development (see, e.g., U.S. Patent Application No. US2001000993183; Caplen et al. Proc Natl Acad Sci U S A; and Abderrahmani et al. Mol Cell Biol 2001 Nov21(21):7256-67).

[0120] An “siRNA” or “RNAi” refers to a nucleic acid that forms a double stranded RNA and has the ability to reduce or inhibit expression of a gene or target gene when the siRNA is delivered to or expressed in the same cell as the gene or target gene. “siRNA” refers to short double-stranded RNA formed by the complementary strands. Complementary portions of the siRNA that hybridize to form the double stranded molecule often have substantial or complete identity to the target molecule sequence. In one embodiment, an siRNA refers to a nucleic acid that has substantial or complete identity to a target gene and forms a double stranded siRNA.

[0121] When designing the siRNA molecules, the targeted region often is selected from a given DNA sequence beginning 50 to 100 nucleotides downstream of the start codon. See, e.g., Elbashir et al., Methods 26:199-213 (2002). Initially, 5' or 3' UTRs and regions nearby the start codon were avoided assuming that UTR-binding proteins and/or translation initiation complexes may interfere with binding of the siRNP or RISC endonuclease complex. Sometimes regions of the target 23 nucleotides in length conforming to the sequence motif AA(N19)TT (N, an nucleotide), and regions with approximately 30% to 70% G/C-content (often about 50% G/C-content) often are selected. If no suitable sequences are found, the search often is extended using the motif NA(N21). The sequence of the sense siRNA sometimes corresponds to (N19) TT or N21 (position 3 to 23 of the 23-nt motif), respectively. In the latter case, the 3' end of the sense siRNA often is converted to TT. The rationale for this sequence conversion is to generate a symmetric duplex with respect to the sequence composition of the sense and antisense 3' overhangs. The antisense siRNA is synthesized as the complement to position 1 to 21 of the 23-nt motif. Because position 1 of the 23-nt motif is not recognized sequence-specifically by the antisense siRNA, the 3'-most nucleotide residue of the antisense siRNA can be chosen deliberately. However, the penultimate nucleotide of the antisense siRNA (complementary to position 2 of the 23-nt motif) often is complementary to the targeted sequence. For simplifying chemical synthesis, TT often is

utilized. siRNAs corresponding to the target motif NAR(N17)YNN, where R is purine (A,G) and Y is pyrimidine (C,U), often are selected. Respective 21 nucleotide sense and antisense siRNAs often begin with a purine nucleotide and can also be expressed from pol III expression vectors without a change in targeting site. Expression of RNAs from pol III promoters often is efficient when the first transcribed nucleotide is a purine.

[0122] The sequence of the siRNA can correspond to the full length target gene, or a subsequence thereof. Often, the siRNA is about 15 to about 50 nucleotides in length (e.g., each complementary sequence of the double stranded siRNA is 15-50 nucleotides in length, and the double stranded siRNA is about 15-50 base pairs in length, sometimes about 20-30 nucleotides in length or about 20-25 nucleotides in length, e.g., 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides in length. The siRNA sometimes is about 21 nucleotides in length. Methods of using siRNA are well known in the art, and specific siRNA molecules may be purchased from a number of companies including Dharmacon Research, Inc.

[0123] Antisense, ribozyme, RNAi and siRNA nucleic acids can be altered to form modified nucleic acid molecules. The nucleic acids can be altered at base moieties, sugar moieties or phosphate backbone moieties to improve stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of nucleic acid molecules can be modified to generate peptide nucleic acids (see Hyrup et al., *Bioorganic & Medicinal Chemistry* 4 (1): 5-23 (1996)). As used herein, the terms “peptide nucleic acid” or “PNA” refers to a nucleic acid mimic such as a DNA mimic, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of a PNA can allow for specific hybridization to DNA and RNA under conditions of low ionic strength. Synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described, for example, in Hyrup et al., (1996) *supra* and Perry-O’Keefe et al., *Proc. Natl. Acad. Sci.* 93: 14670-675 (1996).

[0124] PNA nucleic acids can be used in prognostic, diagnostic, and therapeutic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, for example, inducing transcription or translation arrest or inhibiting replication. PNA nucleic acid molecules can also be used in the analysis of single base pair mutations in a gene, (e.g., by PNA-directed PCR clamping); as “artificial restriction enzymes” when used in combination with other enzymes, (e.g., S1 nucleases (Hyrup (1996) *supra*)); or as probes or primers for DNA sequencing or hybridization (Hyrup et al., (1996) *supra*; Perry-O’Keefe *supra*).

[0125] In other embodiments, oligonucleotides may include other appended groups such as peptides (e.g., for targeting host cell receptors *in vivo*), or agents facilitating transport across cell membranes (see e.g., Letsinger et al., *Proc. Natl. Acad. Sci. USA* 86: 6553-6556 (1989); Lemaitre et al., *Proc. Natl. Acad. Sci. USA* 84: 648-652 (1987); PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization-

triggered cleavage agents (See, e.g., Krol et al., Bio-Techniques 6: 958-976 (1988)) or intercalating agents. (See, e.g., Zon, Pharm. Res. 5: 539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule, (e.g., a peptide, hybridization triggered cross-linking agent, transport agent, or hybridization-triggered cleavage agent).

[0126] Also included herein are molecular beacon oligonucleotide primer and probe molecules having one or more regions complementary to a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A, or a substantially identical sequence thereof, two complementary regions one having a fluorophore and one a quencher such that the molecular beacon is useful for quantifying the presence of the nucleic acid in a sample. Molecular beacon nucleic acids are described, for example, in Lizardi et al., U.S. Patent No. 5,854,033; Nazarenko et al., U.S. Patent No. 5,866,336, and Livak et al., U.S. Patent 5,876,930.

Antibodies

[0127] The term “antibody” as used herein refers to an immunoglobulin molecule or immunologically active portion thereof, i.e., an antigen-binding portion. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and F(ab')₂ fragments which can be generated by treating the antibody with an enzyme such as pepsin. An antibody sometimes is a polyclonal, monoclonal, recombinant (e.g., a chimeric or humanized), fully human, non-human (e.g., murine), or a single chain antibody. An antibody may have effector function and can fix complement, and is sometimes coupled to a toxin or imaging agent.

[0128] A full-length polypeptide or antigenic peptide fragment encoded by a nucleotide sequence referenced herein can be used as an immunogen or can be used to identify antibodies made with other immunogens, e.g., cells, membrane preparations, and the like. An antigenic peptide often includes at least 8 amino acid residues of the amino acid sequences encoded by a nucleotide sequence referenced herein, or substantially identical sequence thereof, and encompasses an epitope. Antigenic peptides sometimes include 10 or more amino acids, 15 or more amino acids, 20 or more amino acids, or 30 or more amino acids. Hydrophilic and hydrophobic fragments of polypeptides sometimes are used as immunogens.

[0129] Epitopes encompassed by the antigenic peptide are regions located on the surface of the polypeptide (e.g., hydrophilic regions) as well as regions with high antigenicity. For example, an Emini surface probability analysis of the human polypeptide sequence can be used to indicate the regions that have a particularly high probability of being localized to the surface of the polypeptide and are thus likely to constitute surface residues useful for targeting antibody production. The antibody may bind an epitope on any domain or region on polypeptides described herein.

[0130] Also, chimeric, humanized, and completely human antibodies are useful for applications which include repeated administration to subjects. Chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, can be made using standard recombinant DNA techniques. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in Robinson et al International Application No. PCT/US86/02269; Akira, et al European Patent Application 184,187; Taniguchi, M., European Patent Application 171,496; Morrison et al European Patent Application 173,494; Neuberger et al PCT International Publication No. WO 86/01533; Cabilly et al U.S. Patent No. 4,816,567; Cabilly et al European Patent Application 125,023; Better et al., Science 240: 1041-1043 (1988); Liu et al., Proc. Natl. Acad. Sci. USA 84: 3439-3443 (1987); Liu et al., J. Immunol. 139: 3521-3526 (1987); Sun et al., Proc. Natl. Acad. Sci. USA 84: 214-218 (1987); Nishimura et al., Canc. Res. 47: 999-1005 (1987); Wood et al., Nature 314: 446-449 (1985); and Shaw et al., J. Natl. Cancer Inst. 80: 1553-1559 (1988); Morrison, S. L., Science 229: 1202-1207 (1985); Oi et al., BioTechniques 4: 214 (1986); Winter U.S. Patent 5,225,539; Jones et al., Nature 321: 552-525 (1986); Verhoeyan et al., Science 239: 1534; and Beidler et al., J. Immunol. 141: 4053-4060 (1988).

[0131] Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Such antibodies can be produced using transgenic mice that are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. See, for example, Lonberg and Huszar, Int. Rev. Immunol. 13: 65-93 (1995); and U.S. Patent Nos. 5,625,126; 5,633,425; 5,569,825; 5,661,016; and 5,545,806. In addition, companies such as Abgenix, Inc. (Fremont, CA) and Medarex, Inc. (Princeton, NJ), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above. Completely human antibodies that recognize a selected epitope also can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody (e.g., a murine antibody) is used to guide the selection of a completely human antibody recognizing the same epitope. This technology is described for example by Jespers et al., Bio/Technology 12: 899-903 (1994).

[0132] An antibody can be a single chain antibody. A single chain antibody (scFV) can be engineered (see, e.g., Colcher et al., Ann. N Y Acad. Sci. 880: 263-80 (1999); and Reiter, Clin. Cancer Res. 2: 245-52 (1996)). Single chain antibodies can be dimerized or multimerized to generate multivalent antibodies having specificities for different epitopes of the same target polypeptide.

[0133] Antibodies also may be selected or modified so that they exhibit reduced or no ability to bind an Fc receptor. For example, an antibody may be an isotype or subtype, fragment or other mutant, which does not support binding to an Fc receptor (e.g., it has a mutagenized or deleted Fc receptor binding region).

[0134] Also, an antibody (or fragment thereof) may be conjugated to a therapeutic moiety such as a cytotoxin, a therapeutic agent or a radioactive metal ion. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1 dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thiotepa chlorambucil, melphalan, carmustine (BCNU) and lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine).

[0135] Antibody conjugates can be used for modifying a given biological response. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a polypeptide such as tumor necrosis factor, gamma-interferon, alpha-interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophage colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors. Also, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Patent No. 4,676,980, for example.

[0136] An antibody (e.g., monoclonal antibody) can be used to isolate target polypeptides by standard techniques, such as affinity chromatography or immunoprecipitation. Moreover, an antibody can be used to detect a target polypeptide (e.g., in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the polypeptide. Antibodies can be used diagnostically to monitor polypeptide levels in tissue as part of a clinical testing procedure, e.g., to determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance (i.e., antibody labeling). Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol;

examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H . Also, an antibody can be utilized as a test molecule for determining whether it can treat osteoarthritis, and as a therapeutic for administration to a subject for treating osteoarthritis.

[0137] An antibody can be made by immunizing with a purified antigen, or a fragment thereof, e.g., a fragment described herein, a membrane associated antigen, tissues, e.g., crude tissue preparations, whole cells, preferably living cells, lysed cells, or cell fractions.

[0138] Included herein are antibodies which bind only a native polypeptide, only denatured or otherwise non-native polypeptide, or which bind both, as well as those having linear or conformational epitopes. Conformational epitopes sometimes can be identified by selecting antibodies that bind to native but not denatured polypeptide. Also featured are antibodies that specifically bind to a polypeptide variant associated with osteoarthritis.

Methods for Identifying Candidate Therapeutics for Treating Osteoarthritis

[0139] Current therapies for the treatment of osteoarthritis have limited efficacy, limited tolerability and significant mechanism-based side effects, and few of the available therapies adequately address underlying defects. Current therapeutic approaches were largely developed in the absence of defined molecular targets or even a solid understanding of disease pathogenesis. Therefore, provided are methods of identifying candidate therapeutics that target biochemical pathways related to the development of osteoarthritis.

[0140] Thus, featured herein are methods for identifying a candidate therapeutic for treating osteoarthritis. The methods comprise contacting a test molecule with a target molecule in a system. A “target molecule” as used herein refers to a *KIAA0296*, *chrom 4* or *SNW1* nucleic acid or other nucleotide sequence referenced in Table A, a substantially identical nucleic acid thereof, or a fragment thereof, and an encoded polypeptide of the foregoing. The methods also comprise determining the presence or absence of an interaction between the test molecule and the target molecule, where the presence of an interaction between the test molecule and the nucleic acid or polypeptide identifies the test molecule as a candidate osteoarthritis therapeutic. The interaction between the test molecule and the target molecule may be quantified.

[0141] Test molecules and candidate therapeutics include, but are not limited to, compounds, antisense nucleic acids, siRNA molecules, ribozymes, polypeptides or proteins encoded by a *KIAA0296*, *chrom 4* or *SNW1* nucleotide sequence or other nucleotide sequence referenced in Table A, or a substantially identical sequence or fragment thereof, and immunotherapeutics (e.g., antibodies and HLA-presented polypeptide fragments). A test molecule or candidate therapeutic may act as a modulator of target molecule concentration or target molecule function in a system. A “modulator” may agonize (i.e.,

up-regulates) or antagonize (i.e., down-regulates) a target molecule concentration partially or completely in a system by affecting such cellular functions as DNA replication and/or DNA processing (e.g., DNA methylation or DNA repair), RNA transcription and/or RNA processing (e.g., removal of intronic sequences and/or translocation of spliced mRNA from the nucleus), polypeptide production (e.g., translation of the polypeptide from mRNA), and/or polypeptide post-translational modification (e.g., glycosylation, phosphorylation, and proteolysis of pro-polypeptides). A modulator may also agonize or antagonize a biological function of a target molecule partially or completely, where the function may include adopting a certain structural conformation, interacting with one or more binding partners, ligand binding, catalysis (e.g., phosphorylation, dephosphorylation, hydrolysis, methylation, and isomerization), and an effect upon a cellular event (e.g., effecting progression of osteoarthritis).

[0142] As used herein, the term “system” refers to a cell free *in vitro* environment and a cell-based environment such as a collection of cells, a tissue, an organ, or an organism. A system is “contacted” with a test molecule in a variety of manners, including adding molecules in solution and allowing them to interact with one another by diffusion, cell injection, and any administration routes in an animal. As used herein, the term “interaction” refers to an effect of a test molecule on test molecule, where the effect sometimes is binding between the test molecule and the target molecule, and sometimes is an observable change in cells, tissue, or organism.

[0143] There are many standard methods for detecting the presence or absence of interaction between a test molecule and a target molecule. For example, titrametric, acidimetric, radiometric, NMR, monolayer, polarographic, spectrophotometric, fluorescent, and ESR assays probative of a target molecule interaction may be utilized. Any modulator can be tested in such methods and modulators for certain targets described in Table A are known. For example, modulators of protein tyrosine phosphatases (e.g., *PTPNI* includes a protein phosphatase domain) are described in WO-03072537, WO-03020688, WO-00218321, WO-00218323, WO-03055883, WO-03041729, WO-00226707, WO-00226743 and WO-03037328; modulators of potassium channels (e.g., *KCNSI* includes a potassium channel domain) are described in WO-09962891, WO-09716437, WO-09521813, WO-09521823, WO-09521824, WO-09521825 and WO-03088908; modulators of annexin (e.g., *ANXA6* includes an annexin domain) are described in WO-2004018670, WO-02067857, WO-2004013303 and WO-00147510; and modulators of protein kinases (e.g., *FYN* is a protein kinase) are described in WO-03081210, WO-02080926, WO-02076986, WO-03077921, WO03026666, WO03026665 and WO03026664.

[0144] Test molecule/target molecule interactions can be detected and/or quantified using assays known in the art. For example, an interaction can be determined by labeling the test molecule and/or the target molecule, where the label is covalently or non-covalently attached to the test molecule or target molecule. The label is sometimes a radioactive molecule such as ^{125}I , ^{131}I , ^{35}S or ^3H , which can be detected by direct counting of radioemission or by scintillation counting. Also, enzymatic labels such as

horseradish peroxidase, alkaline phosphatase, or luciferase may be utilized where the enzymatic label can be detected by determining conversion of an appropriate substrate to product. In addition, presence or absence of an interaction can be determined without labeling. For example, a microphysiometer (*e.g.*, Cytosensor) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indication of an interaction between a test molecule and target molecule (McConnell, H. M. *et al.*, *Science* 257: 1906-1912 (1992)).

[0145] In cell-based systems, cells typically include a *KIAA0296*, *chrom 4* or *SNW1* nucleic acid or other nucleotide sequence referenced in Table A, an encoded polypeptide, or substantially identical nucleic acid or polypeptide thereof, and are often of mammalian origin, although the cell can be of any origin. Whole cells, cell homogenates, and cell fractions (*e.g.*, cell membrane fractions) can be subjected to analysis. Where interactions between a test molecule with a target polypeptide are monitored, soluble and/or membrane bound forms of the polypeptide may be utilized. Where membrane-bound forms of the polypeptide are used, it may be desirable to utilize a solubilizing agent. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton® X-100, Triton® X-114, Thesit®, Isotridecypoly(ethylene glycol ether)_n, 3-[(3-cholamidopropyl)dimethylamminio]-1-propane sulfonate (CHAPS), 3-[(3-cholamidopropyl)dimethylamminio]-2-hydroxy-1-propane sulfonate (CHAPSO), or N-dodecyl-N,N-dimethyl-3-ammonio-1-propane sulfonate.

[0146] An interaction between a test molecule and target molecule also can be detected by monitoring fluorescence energy transfer (FET) (*see, e.g.*, Lakowicz *et al.*, U.S. Patent No. 5,631,169; Stavrianopoulos *et al.* U.S. Patent No. 4,868,103). A fluorophore label on a first, “donor” molecule is selected such that its emitted fluorescent energy will be absorbed by a fluorescent label on a second, “acceptor” molecule, which in turn is able to fluoresce due to the absorbed energy. Alternately, the “donor” polypeptide molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the “acceptor” molecule label may be differentiated from that of the “donor”. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, the spatial relationship between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the “acceptor” molecule label in the assay should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (*e.g.*, using a fluorimeter).

[0147] In another embodiment, determining the presence or absence of an interaction between a test molecule and a target molecule can be effected by monitoring surface plasmon resonance (*see, e.g.*, Sjolander & Urbanicz, *Anal. Chem.* 63: 2338-2345 (1991) and Szabo *et al.*, *Curr. Opin. Struct. Biol.* 5:

699-705 (1995)). “Surface plasmon resonance” or “biomolecular interaction analysis (BIA)” can be utilized to detect biospecific interactions in real time, without labeling any of the interactants (*e.g.*, BIAcore). Changes in the mass at the binding surface (indicative of a binding event) result in alterations of the refractive index of light near the surface (the optical phenomenon of surface plasmon resonance (SPR)), resulting in a detectable signal which can be used as an indication of real-time reactions between biological molecules.

[0148] In another embodiment, the target molecule or test molecules are anchored to a solid phase, facilitating the detection of target molecule/test molecule complexes and separation of the complexes from free, uncomplexed molecules. The target molecule or test molecule is immobilized to the solid support. In an embodiment, the target molecule is anchored to a solid surface, and the test molecule, which is not anchored, can be labeled, either directly or indirectly, with detectable labels discussed herein.

[0149] It may be desirable to immobilize a target molecule, an anti-target molecule antibody, and/or test molecules to facilitate separation of target molecule/test molecule complexes from uncomplexed forms, as well as to accommodate automation of the assay. The attachment between a test molecule and/or target molecule and the solid support may be covalent or non-covalent (*see, e.g.*, U.S. Patent No. 6,022,688 for non-covalent attachments). The solid support may be one or more surfaces of the system, such as one or more surfaces in each well of a microtiter plate, a surface of a silicon wafer, a surface of a bead (*see, e.g.*, Lam, *Nature* 354: 82-84 (1991)) that is optionally linked to another solid support, or a channel in a microfluidic device, for example. Types of solid supports, linker molecules for covalent and non-covalent attachments to solid supports, and methods for immobilizing nucleic acids and other molecules to solid supports are well known (*see, e.g.*, U.S. Patent Nos. 6,261,776; 5,900,481; 6,133,436; and 6,022,688; and WIPO publication WO 01/18234).

[0150] In an embodiment, target molecule may be immobilized to surfaces via biotin and streptavidin. For example, biotinylated target polypeptide can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In another embodiment, a target polypeptide can be prepared as a fusion polypeptide. For example, glutathione-S-transferase/target polypeptide fusion can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivitized microtiter plates, which are then combined with a test molecule under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, or the matrix is immobilized in the case of beads, and complex formation is determined directly or indirectly as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of target molecule binding or activity is determined using standard techniques.

[0151] In an embodiment, the non-immobilized component is added to the coated surface containing the anchored component. After the reaction is complete, unreacted components are removed (*e.g.*, by washing) under conditions such that a significant percentage of complexes formed will remain immobilized to the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of manners. Where the previously non-immobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the previously non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface, *e.g.*, by adding a labeled antibody specific for the immobilized component, where the antibody, in turn, can be directly labeled or indirectly labeled with, *e.g.*, a labeled anti-Ig antibody.

[0152] In another embodiment, an assay is performed utilizing antibodies that specifically bind target molecule or test molecule but do not interfere with binding of the target molecule to the test molecule. Such antibodies can be derivitized to a solid support, and unbound target molecule may be immobilized by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the target molecule, as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the target molecule.

[0153] Cell free assays also can be conducted in a liquid phase. In such an assay, reaction products are separated from unreacted components, by any of a number of standard techniques, including but not limited to: differential centrifugation (*see, e.g.*, Rivas, G., and Minton, *Trends Biochem Sci Aug; 18(8): 284-7 (1993)*); chromatography (gel filtration chromatography, ion-exchange chromatography); electrophoresis (*see, e.g.*, Ausubel *et al., eds. Current Protocols in Molecular Biology*, J. Wiley: New York (1999)); and immunoprecipitation (*see, e.g.*, Ausubel *et al., eds., supra*). Media and chromatographic techniques are known to one skilled in the art (*see, e.g.*, Heegaard, *J Mol. Recognit. Winter; 11(1-6): 141-8 (1998)*; Hage & Tweed, *J. Chromatogr. B Biomed. Sci. Appl. Oct 10; 699 (1-2): 499-525 (1997)*). Further, fluorescence energy transfer may also be conveniently utilized, as described herein, to detect binding without further purification of the complex from solution.

[0154] In another embodiment, modulators of target molecule expression are identified. For example, a cell or cell free mixture is contacted with a candidate compound and the expression of target mRNA or target polypeptide is evaluated relative to the level of expression of target mRNA or target polypeptide in the absence of the candidate compound. When expression of target mRNA or target polypeptide is greater in the presence of the candidate compound than in its absence, the candidate compound is identified as an agonist of target mRNA or target polypeptide expression. Alternatively, when expression of target mRNA or target polypeptide is less (*e.g.*, less with statistical significance) in the presence of the candidate compound than in its absence, the candidate compound is identified as an

antagonist or inhibitor of target mRNA or target polypeptide expression. The level of target mRNA or target polypeptide expression can be determined by methods described herein.

[0155] In another embodiment, binding partners that interact with a target molecule are detected. The target molecules can interact with one or more cellular or extracellular macromolecules, such as polypeptides *in vivo*, and these interacting molecules are referred to herein as “binding partners.” Binding partners can agonize or antagonize target molecule biological activity. Also, test molecules that agonize or antagonize interactions between target molecules and binding partners can be useful as therapeutic molecules as they can up-regulate or down-regulated target molecule activity *in vivo* and thereby treat osteoarthritis.

[0156] Binding partners of target molecules can be identified by methods known in the art. For example, binding partners may be identified by lysing cells and analyzing cell lysates by electrophoretic techniques. Alternatively, a two-hybrid assay or three-hybrid assay can be utilized (*see, e.g.*, U.S. Patent No. 5,283,317; Zervos *et al.*, *Cell* 72:223-232 (1993); Madura *et al.*, *J. Biol. Chem.* 268: 12046-12054 (1993); Bartel *et al.*, *Biotechniques* 14: 920-924 (1993); Iwabuchi *et al.*, *Oncogene* 8: 1693-1696 (1993); and Brent WO94/10300). A two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. The assay often utilizes two different DNA constructs. In one construct, a *KIAA0296*, *chrom 4* or *SNW1* nucleic acid or other nucleic acid referenced in Table A (sometimes referred to as the “bait”) is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In another construct, a DNA sequence from a library of DNA sequences that encodes a potential binding partner (sometimes referred to as the “prey”) is fused to a gene that encodes an activation domain of the known transcription factor. Sometimes, a *KIAA0296*, *chrom 4* or *SNW1* nucleic acid or other nucleic acid referenced in Table A can be fused to the activation domain. If the “bait” and the “prey” molecules interact *in vivo*, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to identify the potential binding partner.

[0157] In an embodiment for identifying test molecules that antagonize or agonize complex formation between target molecules and binding partners, a reaction mixture containing the target molecule and the binding partner is prepared, under conditions and for a time sufficient to allow complex formation. The reaction mixture often is provided in the presence or absence of the test molecule. The test molecule can be included initially in the reaction mixture, or can be added at a time subsequent to the addition of the target molecule and its binding partner. Control reaction mixtures are incubated without the test molecule or with a placebo. Formation of any complexes between the target molecule and the

binding partner then is detected. Decreased formation of a complex in the reaction mixture containing test molecule as compared to in a control reaction mixture indicates that the molecule antagonizes target molecule/binding partner complex formation. Alternatively, increased formation of a complex in the reaction mixture containing test molecule as compared to in a control reaction mixture indicates that the molecule agonizes target molecule/binding partner complex formation. In another embodiment, complex formation of target molecule/binding partner can be compared to complex formation of mutant target molecule/binding partner (*e.g.*, amino acid modifications in a target polypeptide). Such a comparison can be important in those cases where it is desirable to identify test molecules that modulate interactions of mutant but not non-mutated target gene products.

[0158] The assays can be conducted in a heterogeneous or homogeneous format. In heterogeneous assays, target molecule and/or the binding partner are immobilized to a solid phase, and complexes are detected on the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the molecules being tested. For example, test compounds that agonize target molecule/binding partner interactions can be identified by conducting the reaction in the presence of the test molecule in a competition format. Alternatively, test molecules that agonize preformed complexes, *e.g.*, molecules with higher binding constants that displace one of the components from the complex, can be tested by adding the test compound to the reaction mixture after complexes have been formed.

[0159] In a heterogeneous assay embodiment, the target molecule or the binding partner is anchored onto a solid surface (*e.g.*, a microtiter plate), while the non-anchored species is labeled, either directly or indirectly. The anchored molecule can be immobilized by non-covalent or covalent attachments. Alternatively, an immobilized antibody specific for the molecule to be anchored can be used to anchor the molecule to the solid surface. The partner of the immobilized species is exposed to the coated surface with or without the test molecule. After the reaction is complete, unreacted components are removed (*e.g.*, by washing) such that a significant portion of any complexes formed will remain immobilized on the solid surface. Where the non-immobilized species is pre-labeled, the detection of label immobilized on the surface is indicative of complex. Where the non-immobilized species is not pre-labeled, an indirect label can be used to detect complexes anchored to the surface; *e.g.*, by using a labeled antibody specific for the initially non-immobilized species. Depending upon the order of addition of reaction components, test compounds that inhibit complex formation or that disrupt preformed complexes can be detected.

[0160] In another embodiment, the reaction can be conducted in a liquid phase in the presence or absence of test molecule, where the reaction products are separated from unreacted components, and the complexes are detected (*e.g.*, using an immobilized antibody specific for one of the binding components to anchor any complexes formed in solution, and a labeled antibody specific for the other partner to

detect anchored complexes). Again, depending upon the order of addition of reactants to the liquid phase, test compounds that inhibit complex or that disrupt preformed complexes can be identified.

[0161] In an alternate embodiment, a homogeneous assay can be utilized. For example, a preformed complex of the target gene product and the interactive cellular or extracellular binding partner product is prepared. One or both of the target molecule or binding partner is labeled, and the signal generated by the label(s) is quenched upon complex formation (*e.g.*, U.S. Patent No. 4,109,496 that utilizes this approach for immunoassays). Addition of a test molecule that competes with and displaces one of the species from the preformed complex will result in the generation of a signal above background. In this way, test substances that disrupt target molecule/binding partner complexes can be identified.

[0162] Candidate therapeutics for treating osteoarthritis are identified from a group of test molecules that interact with a target molecule. Test molecules are normally ranked according to the degree with which they modulate (*e.g.*, agonize or antagonize) a function associated with the target molecule (*e.g.*, DNA replication and/or processing, RNA transcription and/or processing, polypeptide production and/or processing, and/or biological function/activity), and then top ranking modulators are selected. Also, pharmacogenomic information described herein can determine the rank of a modulator. The top 10% of ranked test molecules often are selected for further testing as candidate therapeutics, and sometimes the top 15%, 20%, or 25% of ranked test molecules are selected for further testing as candidate therapeutics. Candidate therapeutics typically are formulated for administration to a subject.

Therapeutic Formulations

[0163] Formulations and pharmaceutical compositions typically include in combination with a pharmaceutically acceptable carrier one or more target molecule modulators. The modulator often is a test molecule identified as having an interaction with a target molecule by a screening method described above. The modulator may be a compound, an antisense nucleic acid, a ribozyme, an antibody, or a binding partner. Also, formulations may comprise a target polypeptide or fragment thereof in combination with a pharmaceutically acceptable carrier.

[0164] As used herein, the term “pharmaceutically acceptable carrier” includes solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Supplementary active compounds can also be incorporated into the compositions. Pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

[0165] A pharmaceutical composition typically is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application

can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerin, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

[0166] Oral compositions generally include an inert diluent or an edible carrier. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules, *e.g.*, gelatin capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

[0167] Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It should be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

[0168] Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as

required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[0169] For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

[0170] Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art. Molecules can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

[0171] In one embodiment, active molecules are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. Materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

[0172] It is advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier.

[0173] Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the

population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD_{50}/ED_{50} . Molecules which exhibit high therapeutic indices are preferred. While molecules that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

[0174] The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such molecules lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any molecules used in the methods described herein, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC_{50} (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

[0175] As defined herein, a therapeutically effective amount of protein or polypeptide (*i.e.*, an effective dosage) ranges from about 0.001 to 30 mg/kg body weight, sometimes about 0.01 to 25 mg/kg body weight, often about 0.1 to 20 mg/kg body weight, and more often about 1 to 10 mg/kg, 2 to 9 mg/kg, 3 to 8 mg/kg, 4 to 7 mg/kg, or 5 to 6 mg/kg body weight. The protein or polypeptide can be administered one time per week for between about 1 to 10 weeks, sometimes between 2 to 8 weeks, often between about 3 to 7 weeks, and more often for about 4, 5, or 6 weeks. The skilled artisan will appreciate that certain factors may influence the dosage and timing required to effectively treat a subject, including but not limited to the severity of the disease or disorder, previous treatments, the general health and/or age of the subject, and other diseases present. Moreover, treatment of a subject with a therapeutically effective amount of a protein, polypeptide, or antibody can include a single treatment or, preferably, can include a series of treatments.

[0176] With regard to polypeptide formulations, featured herein is a method for treating osteoarthritis in a subject, which comprises contacting one or more cells in the subject with a first polypeptide, where the subject comprises a second polypeptide having one or more polymorphic variations associated with cancer, and where the first polypeptide comprises fewer polymorphic variations associated with cancer than the second polypeptide. The first and second polypeptides are encoded by a nucleic acid which comprises a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A; a nucleotide sequence which encodes a polypeptide consisting of an amino acid sequence encoded by a nucleotide sequence referenced in SEQ ID NO: 1-3 or referenced in Table A; a nucleotide sequence which encodes a polypeptide that is 90% or more identical to an amino acid sequence encoded

by a nucleotide sequence of SEQ ID NO: 1-3 or referenced in Table A and a nucleotide sequence 90% or more identical to a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A. The subject often is a human.

[0177] For antibodies, a dosage of 0.1 mg/kg of body weight (generally 10 mg/kg to 20 mg/kg) is often utilized. If the antibody is to act in the brain, a dosage of 50 mg/kg to 100 mg/kg is often appropriate. Generally, partially human antibodies and fully human antibodies have a longer half-life within the human body than other antibodies. Accordingly, lower dosages and less frequent administration is often possible. Modifications such as lipidation can be used to stabilize antibodies and to enhance uptake and tissue penetration (*e.g.*, into the brain). A method for lipidation of antibodies is described by Cruikshank *et al.*, *J. Acquired Immune Deficiency Syndromes and Human Retrovirology* 14:193 (1997).

[0178] Antibody conjugates can be used for modifying a given biological response, the drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a polypeptide such as tumor necrosis factor, alpha-interferon, beta-interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophage colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors. Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Patent No. 4,676,980.

[0179] For compounds, exemplary doses include milligram or microgram amounts of the compound per kilogram of subject or sample weight, for example, about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1 microgram per kilogram to about 50 micrograms per kilogram. It is understood that appropriate doses of a small molecule depend upon the potency of the small molecule with respect to the expression or activity to be modulated. When one or more of these small molecules is to be administered to an animal (*e.g.*, a human) in order to modulate expression or activity of a polypeptide or nucleic acid described herein, a physician, veterinarian, or researcher may, for example, prescribe a relatively low dose at first, subsequently increasing the dose until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular animal subject will depend upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the degree of expression or activity to be modulated.

[0180] With regard to nucleic acid formulations, gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (*see, e.g.*, U.S. Patent 5,328,470) or by stereotactic injection (*see e.g.*, Chen *et al.*, (1994) *Proc. Natl. Acad. Sci. USA* 91:3054-3057). Pharmaceutical preparations of gene therapy vectors can include a gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells (*e.g.*, retroviral vectors) the pharmaceutical preparation can include one or more cells which produce the gene delivery system. Examples of gene delivery vectors are described herein.

Therapeutic Methods

[0181] A therapeutic formulation described above can be administered to a subject in need of a therapeutic for inducing a desired biological response. Therapeutic formulations can be administered by any of the paths described herein. With regard to both prophylactic and therapeutic methods of treatment, such treatments may be specifically tailored or modified, based on knowledge obtained from pharmacogenomic analyses described herein.

[0182] As used herein, the term “treatment” is defined as the application or administration of a therapeutic formulation to a subject, or application or administration of a therapeutic agent to an isolated tissue or cell line from a subject with the purpose to cure, heal, alleviate, relieve, alter, remedy, ameliorate, improve or affect osteoarthritis, symptoms of osteoarthritis or a predisposition towards osteoarthritis. A therapeutic formulation includes, but is not limited to, small molecules, peptides, antibodies, ribozymes and antisense oligonucleotides. Administration of a therapeutic formulation can occur prior to the manifestation of symptoms characteristic of osteoarthritis, such that osteoarthritis is prevented or delayed in its progression. The appropriate therapeutic composition can be determined based on screening assays described herein.

[0183] As discussed, successful treatment of osteoarthritis can be brought about by techniques that serve to agonize target molecule expression or function, or alternatively, antagonize target molecule expression or function. These techniques include administration of modulators that include, but are not limited to, small organic or inorganic molecules; antibodies (including, for example, polyclonal, monoclonal, humanized, anti-idiotypic, chimeric or single chain antibodies, and Fab, F(ab')₂ and Fab expression library fragments, scFV molecules, and epitope-binding fragments thereof); and peptides, phosphopeptides, or polypeptides.

[0184] Further, antisense and ribozyme molecules that inhibit expression of the target gene can also be used to reduce the level of target gene expression, thus effectively reducing the level of target gene activity. Still further, triple helix molecules can be utilized in reducing the level of target gene activity. Antisense, ribozyme and triple helix molecules are discussed above. It is possible that the use of

antisense, ribozyme, and/or triple helix molecules to reduce or inhibit mutant gene expression can also reduce or inhibit the transcription (triple helix) and/or translation (antisense, ribozyme) of mRNA produced by normal target gene alleles, such that the concentration of normal target gene product present can be lower than is necessary for a normal phenotype. In such cases, nucleic acid molecules that encode and express target gene polypeptides exhibiting normal target gene activity can be introduced into cells via gene therapy method. Alternatively, in instances in that the target gene encodes an extracellular polypeptide, it can be preferable to co-administer normal target gene polypeptide into the cell or tissue in order to maintain the requisite level of cellular or tissue target gene activity.

[0185] Another method by which nucleic acid molecules may be utilized in treating or preventing osteoarthritis is use of aptamer molecules specific for target molecules. Aptamers are nucleic acid molecules having a tertiary structure which permits them to specifically bind to ligands (*see, e.g.,* Osborne, *et al., Curr. Opin. Chem. Biol.* 1(1): 5-9 (1997); and Patel, D. J., *Curr. Opin. Chem. Biol. Jun;1(1): 32-46 (1997)*).

[0186] Yet another method of utilizing nucleic acid molecules for osteoarthritis treatment is gene therapy, which can also be referred to as allele therapy. Provided herein is a gene therapy method for treating osteoarthritis in a subject, which comprises contacting one or more cells in the subject or from the subject with a nucleic acid having a first nucleotide sequence (e.g., the first nucleotide sequence is identical to or substantially identical to a nucleotide sequence of SEQ ID NO: 1-3 or other nucleotide sequence referenced in Table A). Genomic DNA in the subject comprises a second nucleotide sequence having one or more polymorphic variations associated with osteoarthritis (e.g., the second nucleotide sequence is identical to or substantially identical to a nucleotide sequence of SEQ ID NO: 1-3 or other nucleotide sequence referenced in Table A). The first and second nucleotide sequences typically are substantially identical to one another, and the first nucleotide sequence comprises fewer polymorphic variations associated with osteoarthritis than the second nucleotide sequence. The first nucleotide sequence may comprise a gene sequence that encodes a full-length polypeptide or a fragment thereof. The subject is often a human. Allele therapy methods often are utilized in conjunction with a method of first determining whether a subject has genomic DNA that includes polymorphic variants associated with osteoarthritis.

[0187] In another allele therapy embodiment, provided herein is a method which comprises contacting one or more cells in the subject or from the subject with a polypeptide encoded by a nucleic acid having a first nucleotide sequence (e.g., the first nucleotide sequence is identical to or substantially identical to the nucleotide sequence of SEQ ID NO: 1-3 or other nucleotide sequence referenced in Table A). Genomic DNA in the subject comprises a second nucleotide sequence having one or more polymorphic variations associated with osteoarthritis (e.g., the second nucleotide sequence is identical to or substantially identical to a nucleotide sequence of SEQ ID NO: 1-3 or other nucleotide sequence

referenced in Table A). The first and second nucleotide sequences typically are substantially identical to one another, and the first nucleotide sequence comprises fewer polymorphic variations associated with osteoarthritis than the second nucleotide sequence. The first nucleotide sequence may comprise a gene sequence that encodes a full-length polypeptide or a fragment thereof. The subject is often a human.

[0188] For antibody-based therapies, antibodies can be generated that are both specific for target molecules and that reduce target molecule activity. Such antibodies may be administered in instances where antagonizing a target molecule function is appropriate for the treatment of osteoarthritis.

[0189] In circumstances where stimulating antibody production in an animal or a human subject by injection with a target molecule is harmful to the subject, it is possible to generate an immune response against the target molecule by use of anti-idiotypic antibodies (*see, e.g., Herlyn, Ann. Med.; 31(1): 66-78 (1999); and Bhattacharya-Chatterjee & Foon, Cancer Treat. Res.; 94: 51-68 (1998)*). Introducing an anti-idiotypic antibody to a mammal or human subject often stimulates production of anti-anti-idiotypic antibodies, which typically are specific to the target molecule. Vaccines directed to osteoarthritis also may be generated in this fashion.

[0190] In instances where the target molecule is intracellular and whole antibodies are used, internalizing antibodies may be preferred. Lipofectin or liposomes can be used to deliver the antibody or a fragment of the Fab region that binds to the target antigen into cells. Where fragments of the antibody are used, the smallest inhibitory fragment that binds to the target antigen is preferred. For example, peptides having an amino acid sequence corresponding to the Fv region of the antibody can be used. Alternatively, single chain neutralizing antibodies that bind to intracellular target antigens can also be administered. Such single chain antibodies can be administered, for example, by expressing nucleotide sequences encoding single-chain antibodies within the target cell population (*see, e.g., Marasco et al., Proc. Natl. Acad. Sci. USA 90: 7889-7893 (1993)*).

[0191] Modulators can be administered to a patient at therapeutically effective doses to treat osteoarthritis. A therapeutically effective dose refers to an amount of the modulator sufficient to result in amelioration of symptoms of osteoarthritis. Toxicity and therapeutic efficacy of modulators can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.,* for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. Modulators that exhibit large therapeutic indices are preferred. While modulators that exhibit toxic side effects can be used, care should be taken to design a delivery system that targets such molecules to the site of affected tissue in order to minimize potential damage to uninfected cells, thereby reducing side effects.

[0192] Data obtained from cell culture assays and animal studies can be used in formulating a range of dosages for use in humans. The dosage of such compounds lies preferably within a range of

circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage can vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the methods described herein, the therapeutically effective dose can be estimated initially from cell culture assays. A dose can be formulated in animal models to achieve a circulating plasma concentration range that includes the IC₅₀ (*i.e.*, the concentration of the test compound that achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma can be measured, for example, by high performance liquid chromatography.

[0193] Another example of effective dose determination for an individual is the ability to directly assay levels of “free” and “bound” compound in the serum of the test subject. Such assays may utilize antibody mimics and/or “biosensors” that have been created through molecular imprinting techniques. Molecules that modulate target molecule activity are used as a template, or “imprinting molecule”, to spatially organize polymerizable monomers prior to their polymerization with catalytic reagents. The subsequent removal of the imprinted molecule leaves a polymer matrix which contains a repeated “negative image” of the compound and is able to selectively rebind the molecule under biological assay conditions. A detailed review of this technique can be seen in Ansell *et al.*, *Current Opinion in Biotechnology* 7: 89-94 (1996) and in Shea, *Trends in Polymer Science* 2: 166-173 (1994). Such “imprinted” affinity matrixes are amenable to ligand-binding assays, whereby the immobilized monoclonal antibody component is replaced by an appropriately imprinted matrix. An example of the use of such matrixes in this way can be seen in Vlatakis, *et al.*, *Nature* 361: 645-647 (1993). Through the use of isotope-labeling, the “free” concentration of compound which modulates target molecule expression or activity readily can be monitored and used in calculations of IC₅₀. Such “imprinted” affinity matrixes can also be designed to include fluorescent groups whose photon-emitting properties measurably change upon local and selective binding of target compound. These changes readily can be assayed in real time using appropriate fiberoptic devices, in turn allowing the dose in a test subject to be quickly optimized based on its individual IC₅₀. An example of such a “biosensor” is discussed in Kriz *et al.*, *Analytical Chemistry* 67: 2142-2144 (1995).

[0194] The examples set forth below are intended to illustrate but not limit the invention.

Examples

[0195] In the following studies a group of subjects was selected according to specific parameters pertaining to osteoarthritis. Nucleic acid samples obtained from individuals in the study group were subjected to genetic analyses that identified associations between osteoarthritis and certain polymorphic variants in human genomic DNA. The polymorphisms were genotyped again in two replication cohorts consisting of individuals selected for OA. In addition, SNPs proximal to the incident polymorphism in

the *KIAA0296* region, the *SNWI* region and in chromosome 4 were identified and allelotyped in OA case and control pools. Methods are described for producing target polypeptides encoded by the nucleic acids of Table A *in vitro* or *in vivo*, which can be utilized in methods that screen test molecules for those that interact with target polypeptides. Test molecules identified as being interactors with target polypeptides can be screened further as osteoarthritis therapeutics.

Example 1

Samples and Pooling Strategies

Sample Selection

[0196] Blood samples were collected from individuals diagnosed with knee osteoarthritis, which were referred to as case samples. Also, blood samples were collected from individuals not diagnosed with knee osteoarthritis as gender and age-matched controls. A database was created that listed all phenotypic trait information gathered from individuals for each case and control sample. Genomic DNA was extracted from each of the blood samples for genetic analyses.

DNA Extraction from Blood Samples

[0197] Six to ten milliliters of whole blood was transferred to a 50 ml tube containing 27 ml of red cell lysis solution (RCL). The tube was inverted until the contents were mixed. Each tube was incubated for 10 minutes at room temperature and inverted once during the incubation. The tubes were then centrifuged for 20 minutes at 3000 x g and the supernatant was carefully poured off. 100-200 µl of residual liquid was left in the tube and was pipetted repeatedly to resuspend the pellet in the residual supernatant. White cell lysis solution (WCL) was added to the tube and pipetted repeatedly until completely mixed. While no incubation was normally required, the solution was incubated at 37°C or room temperature if cell clumps were visible after mixing until the solution was homogeneous. 2 ml of protein precipitation was added to the cell lysate. The mixtures were vortexed vigorously at high speed for 20 sec to mix the protein precipitation solution uniformly with the cell lysate, and then centrifuged for 10 minutes at 3000 x g. The supernatant containing the DNA was then poured into a clean 15 ml tube, which contained 7 ml of 100% isopropanol. The samples were mixed by inverting the tubes gently until white threads of DNA were visible. Samples were centrifuged for 3 minutes at 2000 x g and the DNA was visible as a small white pellet. The supernatant was decanted and 5 ml of 70% ethanol was added to each tube. Each tube was inverted several times to wash the DNA pellet, and then centrifuged for 1 minute at 2000 x g. The ethanol was decanted and each tube was drained on clean absorbent paper. The DNA was dried in the tube by inversion for 10 minutes, and then 1000 µl of 1X TE was added. The size of each sample was estimated, and less TE buffer was added during the following DNA hydration step if

the sample was smaller. The DNA was allowed to rehydrate overnight at room temperature, and DNA samples were stored at 2-8°C.

[0198] DNA was quantified by placing samples on a hematology mixer for at least 1 hour. DNA was serially diluted (typically 1:80, 1:160, 1:320, and 1:640 dilutions) so that it would be within the measurable range of standards. 125 µl of diluted DNA was transferred to a clear U-bottom microtitre plate, and 125 µl of 1X TE buffer was transferred into each well using a multichannel pipette. The DNA and 1X TE were mixed by repeated pipetting at least 15 times, and then the plates were sealed. 50 µl of diluted DNA was added to wells A5-H12 of a black flat bottom microtitre plate. Standards were inverted six times to mix them, and then 50 µl of 1X TE buffer was pipetted into well A1, 1000 ng/ml of standard was pipetted into well A2, 500 ng/ml of standard was pipetted into well A3, and 250 ng/ml of standard was pipetted into well A4. PicoGreen (Molecular Probes, Eugene, Oregon) was thawed and freshly diluted 1:200 according to the number of plates that were being measured. PicoGreen was vortexed and then 50µl was pipetted into all wells of the black plate with the diluted DNA. DNA and PicoGreen were mixed by pipetting repeatedly at least 10 times with the multichannel pipette. The plate was placed into a Fluoroskan Ascent Machine (microplate fluorometer produced by Labsystems) and the samples were allowed to incubate for 3 minutes before the machine was run using filter pairs 485 nm excitation and 538 nm emission wavelengths. Samples having measured DNA concentrations of greater than 450 ng/µl were re-measured for conformation. Samples having measured DNA concentrations of 20 ng/µl or less were re-measured for confirmation.

Pooling Strategies – Discovery Cohort

[0199] Samples were derived from the Nottingham knee OA family study (UK) where index cases were identified through a knee replacement registry. Siblings were approached and assessed with knee x-rays and assigned status as affected or unaffected. In all 1,157 individuals were available. In order to create same-sex pools of appropriate sizes, 335 unrelated female individuals with OA from the Nottingham OA sample were selected for the case pool. The control pool was made up of unrelated female individuals from the St. Thomas twin study (England) with normal knee x-rays and without other indications of OA, regardless of anatomical location, as well as lacking family history of OA. The St. Thomas twin study consists of Caucasian, female participants from the St. Thomas' Hospital, London, adult-twin registry, which is a voluntary registry of >4,000 twin pairs ranging from 18 to 76 years of age. The female case samples and female control samples are described further in Table 1 below.

[0200] A select set of samples from each group were utilized to generate pools, and one pool was created for each group. Each individual sample in a pool was represented by an equal amount of genomic DNA. For example, where 25 ng of genomic DNA was utilized in each PCR reaction and there

were 200 individuals in each pool, each individual would provide 125 pg of genomic DNA. Inclusion or exclusion of samples for a pool was based upon the following criteria: the sample was derived from an individual characterized as Caucasian; the sample was derived from an individual of British paternal and maternal descent; case samples were derived from individuals diagnosed with specific knee osteoarthritis (OA) and were recruited from an OA knee replacement clinic. Control samples were derived from individuals free of OA, family history of OA, and rheumatoid arthritis. Also, sufficient genomic DNA was extracted from each blood sample for all allelotyping and genotyping reactions performed during the study. Phenotype information from each individual was collected and included age of the individual, gender, family history of OA, general medical information (e.g., height, weight, thyroid disease, diabetes, psoriasis, hysterectomy), joint history (previous and current symptoms, joint-related operations, age at onset of symptoms, date of primary diagnosis, age of individual as of primary diagnosis and order of involvement), and knee-related findings (crepitus, restricted passive movement, bony swelling/deformity). Additional knee information included knee history, current symptoms, any major knee injury, meniscectomy, knee replacement surgery, age of surgery, and treatment history (including hormone replace therapy (HRT)). Samples that met these criteria were added to appropriate pools based on disease status.

[0201] The selection process yielded the pools set forth in Table 1, which were used in the studies that follow:

TABLE 1

	Female case	Female control
Pool size (Number)	335	335
Pool Criteria (ex: case/control)	control	case
Mean Age (ex: years)	57.21	69.95

Example 2

Association of Polymorphic Variants with Osteoarthritis

[0202] A whole-genome screen was performed to identify particular SNPs associated with occurrence of osteoarthritis. As described in Example 1, two sets of samples were utilized, which included samples from female individuals having knee osteoarthritis (osteoarthritis cases), and samples from female individuals not having knee osteoarthritis (female controls). The initial screen of each pool was performed in an allelotyping study, in which certain samples in each group were pooled. By pooling DNA from each group, an allele frequency for each SNP in each group was calculated. These allele

frequencies were then compared to one another. Particular SNPs were considered as being associated with osteoarthritis when allele frequency differences calculated between case and control pools were statistically significant. SNP disease association results obtained from the allelotyping study were then validated by genotyping each associated SNP across all samples from each pool. The results of the genotyping then were analyzed, allele frequencies for each group were calculated from the individual genotyping results, and a p-value was calculated to determine whether the case and control groups had statistically significant differences in allele frequencies for a particular SNP. When the genotyping results agreed with the original allelotyping results, the SNP disease association was considered validated at the genetic level.

SNP Panel Used for Genetic Analyses

[0203] A whole-genome SNP screen began with an initial screen of approximately 25,000 SNPs over each set of disease and control samples using a pooling approach. The pools studied in the screen are described in Example 1. The SNPs analyzed in this study were part of a set of 25,488 SNPs confirmed as being statistically polymorphic as each is characterized as having a minor allele frequency of greater than 10%. The SNPs in the set reside in genes or in close proximity to genes, and many reside in gene exons. Specifically, SNPs in the set are located in exons, introns, and within 5,000 base-pairs upstream of a transcription start site of a gene. In addition, SNPs were selected according to the following criteria: they are located in ESTs; they are located in Locuslink or Ensembl genes; and they are located in Genomatix promoter predictions. SNPs in the set were also selected on the basis of even spacing across the genome, as depicted in Table 2.

[0204] A case-control study design using a whole genome association strategy involving approximately 28,000 single nucleotide polymorphisms (SNPs) was employed. Approximately 25,000 SNPs were evenly spaced in gene-based regions of the human genome with a median inter-marker distance of about 40,000 base pairs. Additionally, approximately 3,000 SNPs causing amino acid substitutions in genes described in the literature as candidates for various diseases were used. The case-control study samples were of female Caucasian origin (British paternal and maternal descent) 670 individuals were equally distributed in two groups: female controls and female cases. The whole genome association approach was first conducted on 2 DNA pools representing the 2 groups. Significant markers were confirmed by individual genotyping.

TABLE 2

<u>General Statistics</u>		<u>Spacing Statistics</u>	
Total # of SNPs	25,488	Median	37,058 bp
# of Exonic SNPs	>4,335 (17%)	Minimum*	1,000 bp
# SNPs with refSNP ID	20,776 (81%)	Maximum*	3,000,000 bp
Gene Coverage	>10,000	Mean	122,412 bp
Chromosome Coverage	All	Std Deviation	373,325 bp
		<i>*Excludes outliers</i>	

Allelotyping and Genotyping Results

[0205] The genetic studies summarized above and described in more detail below identified allelic variants associated with osteoarthritis, which are summarized in Table A.

Assay for Verifying, Allelotyping, and Genotyping SNPs

[0206] A MassARRAY™ system (Sequenom, Inc.) was utilized to perform SNP genotyping in a high-throughput fashion. This genotyping platform was complemented by a homogeneous, single-tube assay method (hME™ or homogeneous MassEXTEND™ (Sequenom, Inc.)) in which two genotyping primers anneal to and amplify a genomic target surrounding a polymorphic site of interest. A third primer (the MassEXTEND™ primer), which is complementary to the amplified target up to but not including the polymorphism, was then enzymatically extended one or a few bases through the polymorphic site and then terminated.

[0207] For each polymorphism, SpectroDESIGNER™ software (Sequenom, Inc.) was used to generate a set of PCR primers and a MassEXTEND™ primer which were used to genotype the polymorphism. Other primer design software could be used or one of ordinary skill in the art could manually design primers based on his or her knowledge of the relevant factors and considerations in designing such primers. Table 3 shows PCR primers and Table 4 shows extension primers used for analyzing polymorphisms. The initial PCR amplification reaction was performed in a 5 µl total volume containing 1X PCR buffer with 1.5 mM MgCl₂ (Qiagen), 200 µM each of dATP, dGTP, dCTP, dTTP (Gibco-BRL), 2.5 ng of genomic DNA, 0.1 units of HotStar DNA polymerase (Qiagen), and 200 nM each of forward and reverse PCR primers specific for the polymorphic region of interest.

TABLE 3: PCR Primers

SNP Reference	Forward PCR primer	Reverse PCR primer
rs552	ACGTTGGATGGACTGAGGTAGATGATGC	ACGTTGGATGGCTTTCTTCCCTTGGTTTC
rs12904	ACGTTGGATGGAACCACTCCCACCACAG	ACGTTGGATGGGTGGGGATGGCACTGTC
rs2282146	ACGTTGGATGTCCCACGAGGACCTGGAG	ACGTTGGATGTTCGTTTGGGTGGCCGGG

SNP Reference	Forward PCR primer	Reverse PCR primer
rs734784	ACGTTGGATGTCGGGATGTCTCCAGAGATG	ACGTTGGATGGCAACCACCAAGAGTTTGAG
rs1042164	ACGTTGGATGTTTCTTCCAGACGGGCTTTC	ACGTTGGATGCAAAGTCAGCCGCAAACGAC
rs749670	ACGTTGGATGTCTCATCTGTGTGCCCATTG	ACGTTGGATGATGAGGGTGAAAGGCAGGAG
rs955592	ACGTTGGATGTTCCCATTCCTTCTTGGGCTC	ACGTTGGATGTCTCAGAGGGTCTCCTTTTC
rs1143016	ACGTTGGATGTTGTCCAGCAGGTAGGGCAG	ACGTTGGATGACCCATCGCGGATACATGTG
rs755248	ACGTTGGATGGGTCTCTGCTGAGGAAGTGG	ACGTTGGATGACACTCACTACGGGGCCAG
rs1055055	ACGTTGGATGTTGTGCTTGCTGAGGAATCC	ACGTTGGATGGTTGCAGAGAGCGTCTATAC
rs835409	ACGTTGGATGTCCTGTTGGCTTTTGCAGAC	ACGTTGGATGACTGCTCATGGTGGTTGAAC
rs927663	ACGTTGGATGTTTGAAGTGGTGGCCCAAC	ACGTTGGATGAAGAATCTTCAGTGCCAGCC
rs8162	ACGTTGGATGCTTCATCCAGAACCTCCAGG	ACGTTGGATGTGCATATGGCTTGTGAGAGC
rs831038	ACGTTGGATGTGAAAGAGCTGCCTTCTTTC	ACGTTGGATGAAATGACACTCACGGTAAGC
rs33079	ACGTTGGATGTTATTTTCATTGGCCAAGCCC	ACGTTGGATGGTGTTCACCTGTTTCATGCAC
rs1710880	ACGTTGGATGCGAAGGCAGAGAATAAACTG	ACGTTGGATGAACTCTGTGGTTTAAAGAAAG
rs1078153	ACGTTGGATGTCCTGCGTGTAACTGAGAGG	ACGTTGGATGAACATACACACAGTGCGAGC
rs799570	ACGTTGGATGATGCATATGGGCAGGTTGCC	ACGTTGGATGCCAGGAAAGCATCCTCAGAC
rs1282730	ACGTTGGATGTCCTTTGACTTACTGTGCTG	ACGTTGGATGAGAAAAGAGGTTGTGTACAG
rs1518875	ACGTTGGATGAGAATGCGTTCAATGCCTGC	ACGTTGGATGAGCGAAAAGCTCTGCCATTG
rs1568694	ACGTTGGATGGTTCATTCAAGTTATGGACGG	ACGTTGGATGTGATAGGAGGGAGCCATCTC
rs905042	ACGTTGGATGTAACAATGGTAAGGGCCAAG	ACGTTGGATGGGTCCATAATGGTCATTGTG
rs1957723	ACGTTGGATGTACTCACTTGTGTACTGCTC	ACGTTGGATGGCTGCAGCGTCACATTAATC
rs794018	ACGTTGGATGGGATGATGATGAAATGACTG	ACGTTGGATGGCTCTAGTTAGATGAGTCTC
rs707723	ACGTTGGATGTGTGGCTGAAGTTTGCTCTG	ACGTTGGATGCACACACAAACCTTGAAGAG
rs893861	ACGTTGGATGGAGGCATGTACACAAAACCTG	ACGTTGGATGGCTCAGCACTGTAATAGTTG
rs1914903	ACGTTGGATGTGCGTCAAGTTGAAGTCCTC	ACGTTGGATGAGGGTAGTGAGTTCACATGC
rs2062232	ACGTTGGATGTCCTGCTCAGATAACTGCTG	ACGTTGGATGGCGGTAGTTTTCCCTAAACC
rs26609	ACGTTGGATGCAAGGGAGATCAGAAACATC	ACGTTGGATGAATTCATTGTTCTTGATGGC
rs1370987	ACGTTGGATGATACTTTGGATGTCTGGTGG	ACGTTGGATGGGTCTTTGGTCACAACATC
rs1012414	ACGTTGGATGACTTGGAAAGTCAGTCTGGG	ACGTTGGATGGAAACCGAGAAATGGCTATG
rs435903	ACGTTGGATGGGCATAAGTTAGAGACAACC	ACGTTGGATGGGCTATGTTATGCTGCTGTG
rs1248	ACGTTGGATGGAGATTGTGCATTTTGGCAAG	ACGTTGGATGCAGACACCATCTTAACCAAG
rs703508	ACGTTGGATGAGCTCTGTGGCCTCTTTTGG	ACGTTGGATGTACTCACAGTCTTCCGGCGG
rs226465	ACGTTGGATGAATTTTGACCCCTGCCAACC	ACGTTGGATGTATGTGAAAGAGGCGGTGAAG
rs241448	ACGTTGGATGCAAGCTGCAGAACGTTGCC	ACGTTGGATGTGAGAAAGAGGGCCAGTATC
rs763155	ACGTTGGATGGGGAACCCAAACTAGTGTG	ACGTTGGATGTACAGGAGAGTAATGCCTC
rs1040461	ACGTTGGATGACATCTGGTGGAAGTCACTC	ACGTTGGATGGGTCTTTGTTTGGGTG
rs462832	ACGTTGGATGCACTTTCTCTGTAATATTTG	ACGTTGGATGTGAGACAACAAAAATTTGCC
rs804194	ACGTTGGATGTAATCCGGTGGCAGATCAAG	ACGTTGGATGGAAATTCATGTGCTGACGGG
rs1022646	ACGTTGGATGACTGTACCTAATCATCCTG	ACGTTGGATGGACTATGTTGGAGTTCAGAG
rs1569112	ACGTTGGATGTCATGATCTGCCTGTGGAGA	ACGTTGGATGACCATCCTCACACCCATCCA
rs805623	ACGTTGGATGATCAACCACTCATACACTGC	ACGTTGGATGCACAGAAACAGCTGGATTGC
rs1019850	ACGTTGGATGTTTTACTCCAGGAAGCCACC	ACGTTGGATGAGCAGGGAGAAATTGTTCCAG
rs1599931	ACGTTGGATGTCAAACCTTCTGTAGACG	ACGTTGGATGTGAACATAGTAGGCGCTCAG
AA	ACGTTGGATGTAGGAGTGCTCGTATTTTGG	ACGTTGGATGCTGGGAACAGCTTTTGATCC
rs279941	ACGTTGGATGCATAGGGAACACCGAGAATG	ACGTTGGATGGGTTGTCTATGTTGGCTAG
rs1062230	ACGTTGGATGAAACTCCTTTCCCTCTCAAG	ACGTTGGATGGGCCATCAGTCTATAGTTT
rs1859911	ACGTTGGATGCTGTTTTCCGAGCATCTAC	ACGTTGGATGCCTCTTGCATATGAGATAGG
rs1477261	ACGTTGGATGCAGGGTTATGTGGTATTATC	ACGTTGGATGGGGAAAGTAAAAGATAAGAG
rs1191119	ACGTTGGATGACTCTCAGGGTGATTATCTG	ACGTTGGATGTGTAAGATTCTGGCACTGTC
rs657780	ACGTTGGATGTTTAAAGAGCCGCCAAGGAG	ACGTTGGATGCCCATTTCAGACCACTTGG
rs1393890	ACGTTGGATGGTCTGATTATCTTCTGCCG	ACGTTGGATGGGTACCTTTATCCTTGCTTC
rs1478714	ACGTTGGATGAATAATTTGCTGACACCCCC	ACGTTGGATGGGAGTCCAGAGGTTAAACAG

SNP Reference	Forward PCR primer	Reverse PCR primer
rs868213	ACGTTGGATGTGTCAGAACTGGGCACATTC	ACGTTGGATGAGGGATAGGGATCAGGAATG
rs690115	ACGTTGGATGAATAGCCAAGGCCGTGTGGG	ACGTTGGATGCACCTGGGAGATAGCAGGG
rs1465501	ACGTTGGATGTCAGGAATTGTTACCTGGAC	ACGTTGGATGCCCTCATCTAGACACTTTTG
rs899173	ACGTTGGATGAGTGCCACATCACTCTTG	ACGTTGGATGTTCTGCTCCACTACAGTCTC
rs10477	ACGTTGGATGGGGGCTACGTGGAAGTTACC	ACGTTGGATGATGGCAATCAAGAGAGTCTAA
rs926393	ACGTTGGATGAGATCAGCCCAGGAAATGTG	ACGTTGGATGTGTTGGAGAAGGTTCCACC
rs465271	ACGTTGGATGAATCACAGCTCATGGCTCAC	ACGTTGGATGATGGTAGTGTGCACCTATGG
rs13847	ACGTTGGATGCGCCCGTAGTGATAAGCAC	ACGTTGGATGCAGGACAGGGCAGAGTGAG
rs738658	ACGTTGGATGGATGGTATGTGTGCATCAGG	ACGTTGGATGCTTCCAAGAGATGGCGTTC

[0208] Samples were incubated at 95°C for 15 minutes, followed by 45 cycles of 95°C for 20 seconds, 56°C for 30 seconds, and 72°C for 1 minute, finishing with a 3 minute final extension at 72°C. Following amplification, shrimp alkaline phosphatase (SAP) (0.3 units in a 2 µl volume) (Amersham Pharmacia) was added to each reaction (total reaction volume was 7 µl) to remove any residual dNTPs that were not consumed in the PCR step. Samples were incubated for 20 minutes at 37°C, followed by 5 minutes at 85°C to denature the SAP.

[0209] Once the SAP reaction was complete, a primer extension reaction was initiated by adding a polymorphism-specific MassEXTEND™ primer cocktail to each sample. Each MassEXTEND™ cocktail included a specific combination of dideoxynucleotides (ddNTPs) and deoxynucleotides (dNTPs) used to distinguish polymorphic alleles from one another. Methods for verifying, allelotyping and genotyping SNPs are disclosed, for example, in U.S. Pat. No. 6,258,538, the content of which is hereby incorporated by reference. In Table 4, ddNTPs are shown and the fourth nucleotide not shown is the dNTP.

TABLE 4: Extension Primers

SNP Reference	Extend Probe	Termination Mix
rs552	TGATGCTGTTGTCAGATACC	ACT
rs12904	AGCCTCAAAACGGGTCA	ACT
rs2282146	GGACCTGGAGCCCCACC	ACG
rs734784	GCCTCCGACACCCCATCAA	ACG
rs1042164	CTTGCTCGGGACCACTCCA	ACT
rs749670	GGTGGTGGGCATCCCTTTC	ACG
rs955592	TTGGGCTCTGACCACCTCT	ACT
rs1143016	ATGCAGCGTCACCAGCAC	ACT
rs755248	TGAGGAAGTGGCAGGTGTG	ACG
rs1055055	CCCAGTTCAGGCTCACTTTC	ACT
rs835409	TTGCAGACCAGCCAATTAAGAA	ACT
rs927663	GGTTGCCCCAACTCCCTT	ACT
rs8162	AACACAGAGCAAAGCACC	ACT
rs831038	CGTTATAGTAAAGGAAAGGCAG	ACG

SNP Reference	Extend Probe	Termination Mix
rs33079	CCCATCACCTGGAGCTTTG	ACG
rs1710880	CTGTATTATGTTTCCCCTTGG	CGT
rs1078153	GCCGGCACCGTCAGAAAC	CGT
rs799570	GCAGTTCCTAGAAGACAGCT	ACT
rs1282730	TGCTGGCCCAACTTTTGTCT	ACG
rs1518875	CTGCAATGTTTCCAAACCCC	ACT
rs1568694	AGTTATGGACGGAAGAAGGG	ACG
rs905042	GGTAAGGGCCAAGTGAGTG	CGT
rs1957723	AGCATGGCATAGGCACTGG	ACG
rs794018	AAATGACTGAAAATGTGACTATA	ACG
rs707723	CCTGAGGTATATTCAATA	ACG
rs893861	CATGTACACAAAAGTGAAGTAA	ACG
rs1914903	TCCCCATAGATGGACCTGC	ACG
rs2062232	GCTGAAGACAAGGATTAGGTT	ACG
rs26609	GAGATCAGAAACATCACCTTG	CGT
rs1370987	TTTGGGAGTTACTGCCTTAGAA	ACT
rs1012414	ACTAGGAACCAGAATATGAGCATC	ACG
rs435903	AAGCTAACAATGGAATAATGGC	ACG
rs1248	GTGCATTTTGGCAAGAATATATG	CGT
rs703508	GGGGTCCAGGCAGAAAGAAAC	ACG
rs226465	CCTCTTCCCCTCCTCCCT	ACT
rs241448	GCAGAAGCTTGCCCAGCTC	ACG
rs763155	GCAGCCTGCAAGTGAGTGA	ACT
rs1040461	AAGTCACTCCGGTCAGAATTCA	ACT
rs462832	ATAAGAATCTTTAGATCCCAACA	CGT
rs804194	GATCAAGGCTGATCTCGCC	ACT
rs1022646	CCTAATCATCCTGCCACCC	ACT
rs1569112	ACCAGGCCGCATGGGCTG	ACG
rs805623	CTGTGTTCAAATAAGGCAACC	ACT
rs1019850	AGGAAGCCACCAGCTAATAC	CGT
rs1599931	CTGAGGCCGGGAGGGATT	ACT
AA	TAGTTTTAAATTCTGCACA	ACT
rs279941	AACACCGAGAATGAAAACATC	ACT
rs1062230	ATGCTGGTTCTGTCCAA	ACG
rs1859911	TCCGAGCATCTACATGCTCA	ACT
rs1477261	AGGAGGAGCCCAATATGAAA	CGT
rs1191119	GTCTTTTGTAACTGGGGAACCC	ACG
rs657780	CGCCAAGGAGTTTCCCACA	ACT
rs1393890	CTGCCGTACCTGGCAAGC	ACT
rs1478714	CCCCGAGGGGACAGTCCA	ACG
rs868213	GGGCACATTCTTGAGGAGGT	ACG
rs690115	AGCCGAGGGAGCTGACCCTG	ACG
rs1465501	TCCAGGAGCCCTCAGAATG	ACT
rs899173	CCTCTGGCAAAGTGTGGAGC	ACG
rs10477	AGTACGATATCAAAGATC	ACG
rs926393	CAGGAAATGTGCTTTCGAGTTCC	ACG
rs465271	GGCTCAAGGGATCCTCCCA	ACG
rs13847	AAGCACACCGGCACGAAC	ACT
rs738658	GAGGCATTTTCATTAATGCATG	CGT

[0210] The MassEXTEND™ reaction was performed in a total volume of 9 µl, with the addition of 1X ThermoSequenase buffer, 0.576 units of ThermoSequenase (Amersham Pharmacia), 600 nM MassEXTEND™ primer, 2 mM of ddATP and/or ddCTP and/or ddGTP and/or ddTTP, and 2 mM of dATP or dCTP or dGTP or dTTP. The deoxy nucleotide (dNTP) used in the assay normally was complementary to the nucleotide at the polymorphic site in the amplicon. Samples were incubated at 94°C for 2 minutes, followed by 55 cycles of 5 seconds at 94°C, 5 seconds at 52°C, and 5 seconds at 72°C.

[0211] Following incubation, samples were desalted by adding 16 µl of water (total reaction volume was 25 µl), 3 mg of SpectroCLEAN™ sample cleaning beads (Sequenom, Inc.) and allowed to incubate for 3 minutes with rotation. Samples were then robotically dispensed using a piezoelectric dispensing device (SpectroJET™ (Sequenom, Inc.)) onto either 96-spot or 384-spot silicon chips containing a matrix that crystallized each sample (SpectroCHIP™ (Sequenom, Inc.)). Subsequently, MALDI-TOF mass spectrometry (Biflex and Autoflex MALDI-TOF mass spectrometers (Bruker Daltonics) can be used) and SpectroTYPER RT™ software (Sequenom, Inc.) were used to analyze and interpret the SNP genotype for each sample.

Genetic Analysis

[0212] Minor allelic frequencies for the polymorphisms set forth in Table A were verified as being 10% or greater using the extension assay described above in a group of samples isolated from 92 individuals originating from the state of Utah in the United States, Venezuela and France (Coriell cell repositories).

[0213] Genotyping results are shown for female pools in Table 5. In Table 5, “AF” refers to allelic frequency; and “F case” and “F control” refer to female case and female control groups, respectively.

TABLE 5: Genotyping Results

SNP Reference	AF F case	AF F control	p-value
rs552	A = 0.190 G = 0.810	A = 0.123 G = 0.877	0.0011
rs12904	A = 0.455 G = 0.545	A = 0.375 G = 0.625	0.0012
rs2282146	C = 0.906 T = 0.094	C = 0.939 T = 0.061	0.0105
rs734784	G = 0.483 A = 0.517	G = 0.416 A = 0.584	0.0052
rs1042164	T = 0.233 C = 0.767	T = 0.159 C = 0.841	0.0002
rs749670	C = 0.342 T = 0.658	C = 0.419 T = 0.581	0.0038
rs955592	T = 0.045 C = 0.955	T = 0.076 C = 0.924	0.0177

SNP Reference	AF F case	AF F control	p-value
rs1143016	T = 0.093 C = 0.907	T = 0.054 C = 0.946	0.0071
rs755248	G = 0.146 A = 0.854	G = 0.069 A = 0.931	0.0000
rs1055055	A = 0.432 G = 0.568	A = 0.355 G = 0.645	0.0046
rs835409	T = 0.620 G = 0.380	T = 0.681 G = 0.319	0.0222
rs927663	T = 0.301 G = 0.699	T = 0.358 G = 0.642	0.0289
rs8162	A = 0.591 G = 0.409	A = 0.657 G = 0.343	0.0149
rs831038	C = 0.617 T = 0.383	C = 0.666 T = 0.334	0.0359
rs33079	G = 0.823 A = 0.177	G = 0.881 A = 0.119	0.0013
rs1710880	C = 0.303 A = 0.697	C = 0.371 A = 0.629	0.0129
rs1078153	T = 0.818 A = 0.182	T = 0.875 A = 0.125	0.0039
rs799570	A = 0.675 G = 0.325	A = 0.740 G = 0.260	0.0100
rs1282730	G = 0.086 A = 0.914	G = 0.127 A = 0.873	0.0150
rs1518875	T = 0.033 C = 0.967	T = 0.055 C = 0.945	0.0508
rs1568694	G = 0.045 A = 0.955	G = 0.081 A = 0.919	0.0064
rs905042	A = 0.832 T = 0.168	A = 0.769 T = 0.231	0.0047
rs1957723	G = 0.778 A = 0.222	G = 0.839 A = 0.161	0.0048
rs794018	G = 0.273 A = 0.727	G = 0.220 A = 0.780	0.0034
rs707723	C = 0.759 T = 0.241	C = 0.811 T = 0.189	0.0195
rs893861	G = 0.246 A = 0.754	G = 0.196 A = 0.804	0.0251
rs1914903	G = 0.861 A = 0.139	G = 0.910 A = 0.090	0.0055
rs2062232	C = 0.064 T = 0.936	C = 0.117 T = 0.883	0.0012
rs26609	A = 0.777 T = 0.223	A = 0.840 T = 0.160	0.0039
rs1370987	A = 0.422 G = 0.578	A = 0.341 G = 0.659	0.0007
rs1012414	G = 0.876 A = 0.124	G = 0.833 A = 0.167	0.0289
rs435903	G = 0.766 A = 0.234	G = 0.685 A = 0.315	0.0013
rs1248	T = 0.668 A = 0.332	T = 0.593 A = 0.407	0.0014
rs703508	G = 0.875 A = 0.125	G = 0.910 A = 0.090	0.0375
rs226465	G = 0.094 C = 0.906	G = 0.129 C = 0.871	0.0454
rs241448	C = 0.294 T = 0.706	C = 0.212 T = 0.788	0.0010
rs763155	A = 0.160	A = 0.114	0.0140

SNP Reference	AF F case	AF F control	p-value
	C = 0.840	C = 0.886	
rs1040461	T = 0.069 C = 0.931	T = 0.098 C = 0.902	0.0281
rs462832	A = 0.218 T = 0.782	A = 0.145 T = 0.855	0.0008
rs804194	T = 0.583 C = 0.417	T = 0.679 C = 0.321	0.0004
rs1022646	A = 0.169 G = 0.831	A = 0.103 G = 0.897	0.0007
rs1569112	G = 0.853 A = 0.147	G = 0.812 A = 0.188	0.0468
rs805623	A = 0.097 G = 0.903	A = 0.140 G = 0.860	0.0143
rs1019850	A = 0.330 T = 0.670	A = 0.240 T = 0.760	0.0005
rs1599931	A = 0.581 G = 0.419	A = 0.659 G = 0.341	0.0037
AA	A = 0.506 G = 0.494	A = 0.577 G = 0.423	0.0102
rs279941	T = 0.100 G = 0.900	T = 0.138 G = 0.862	0.0324
rs1062230	C = 0.778 T = 0.222	C = 0.717 T = 0.283	0.0109
rs1859911	T = 0.295 C = 0.705	T = 0.243 C = 0.757	0.0328
rs1477261	T = 0.861 A = 0.139	T = 0.809 A = 0.191	0.0105
rs1191119	G = 0.121 A = 0.879	G = 0.078 A = 0.922	0.0079
rs657780	A = 0.674 G = 0.326	A = 0.583 G = 0.417	0.0009
rs1393890	G = 0.639 C = 0.361	G = 0.724 C = 0.276	0.0014
rs1478714	G = 0.331 A = 0.669	G = 0.269 A = 0.731	0.0136
rs868213	C = 0.078 T = 0.922	C = 0.044 T = 0.956	0.0083
rs690115	G = 0.839 A = 0.161	G = 0.784 A = 0.216	0.0111
rs1465501	A = 0.846 G = 0.154	A = 0.903 G = 0.097	0.0020
rs899173	C = 0.895 T = 0.105	C = 0.858 T = 0.142	0.0408
rs10477	C = 0.087 T = 0.913	C = 0.146 T = 0.854	0.0010
rs926393	C = 0.715 T = 0.285	C = 0.647 T = 0.353	0.0082
rs465271	C = 0.194 T = 0.806	C = 0.130 T = 0.870	0.0019
rs13847	A = 0.111 G = 0.889	A = 0.163 G = 0.837	0.0056
rs738658	C = 0.898 A = 0.102	C = 0.855 A = 0.145	0.0183

[0214] All of the single marker alleles set forth in Table A were considered validated, since the genotyping data agreed with the allelotyping data and each SNP significantly associated with

osteoarthritis. Particularly significant associations with osteoarthritis are indicated by a calculated p-value of less than 0.05 for genotype results.

Example 3

Association of Polymorphic Variants with Osteoarthritis in Replication Cohorts

[0215] The single marker polymorphisms set forth in Table A were genotyped again in two replication cohorts consisting of individuals selected for OA.

Sample Selection and Pooling Strategies – Replication Sample 1

[0216] A second case control sample (replication sample #1) was created by using 100 Caucasian female cases from Chingford, UK, and 148 unrelated female cases from the St. Thomas twin study. Cases were defined as having Kellgren-Lawrence (KL) scores of at least 2 in at least one knee x-ray. In addition, 199 male knee replacement cases from Nottingham were included. (For a cohort description, see the Nottingham description provided in Example 1). The control pool was made up of unrelated female individuals from the St. Thomas twin study (England) with normal knee x-rays and without other indications of OA, regardless of anatomical location, as well as lacking family history of OA. The St. Thomas twin study consists of Caucasian, female participants from the St. Thomas' Hospital, London, adult-twin registry, which is a voluntary registry of >4,000 twin pairs ranging from 18 to 76 years of age. The replication sample 1 cohort was used to replicate the initial results. Table 6 below summarizes the selected phenotype data collected from the case and control individuals.

TABLE 6

Phenotype	Female cases (n=248): median (range)/ (n,%)	Male cases (n=199): median (range)/ (n,%)	Female controls (n=313): mean (range)/ (n,%)
Age	59 (39- 73)	66 (45- 73)	55 (50- 72)
Height (cm)	162 (141- 178)	175 (152- 198)	162 (141- 176)
Weight (kg)	68 (51- 123)	86 (62- 127)	64 (40- 111)
Body mass index (kg/m ²)	26 (18- 44)	29 (21- 41)	24 (18- 46)
Kellgren-Lawrence* left knee	0 (63, 26%), 1 (20, 8%), 2 (105, 43%), 3 (58, 23%), 4 (1, 0%)	NA	NA
Kellgren-Lawrence* right knee	0 (43, 7%), 1 (18, 7%), 2 (127, 52%), 3 (57, 23%), 4 (1, 0%)	NA	NA
KL* >2 both knees	No (145, 59%), Yes (101, 41%)	NA	NA

Phenotype	Female cases (n=248): median (range)/ (n,%)	Male cases (n=199): median (range)/ (n,%)	Female controls (n=313): mean (range)/ (n,%)
KL* >2 either knee	No (0, 0%), Yes (248, 100%)	NA	NA

* 0: normal, 1: doubtful, 2: definite osteophyte (bony protuberance), 3: joint space narrowing (with or without osteophyte), 4: joint deformity

Sample Selection and Pooling Strategies – Replication Sample 2

[0217] A third case control sample (replication sample #2) was created by using individuals with symptoms of OA from Newfoundland, Canada. These individuals were recruited and examined by rheumatologists. Affected joints were x-rayed and a final diagnosis of definite or probable OA was made according to American College of Rheumatology criteria by a single rheumatologist to avoid any inter-examiner diagnosis variability. Controls were recruited from volunteers without any symptoms from the musculoskeletal system based on a normal joint exam performed by a rheumatologist. Only cases with a diagnosis of definite OA were included in the study. Only individuals of Caucasian origin were included. The cases consisted of 228 individuals with definite knee OA, 106 individuals with definite hip OA, and 74 individuals with hip OA.

TABLE 7

Phenotype	Case	Control
Age at Visit	62.7	52.5
Sex (Female/Male)	227/119	174/101
Knee OA Xray: No	35% (120)	80% (16)
Unknown	1% (4)	0% (0)
Yes	64% (221)	20% (4)
Hip OA Xray: No	63% (215)	80% (16)
Unknown	2% (7)	0% (0)
Yes	35% (121)	20% (4)

Assay for Verifying, Allelotyping, and Genotyping SNPs

[0218] Genotyping of the replication cohorts described in Tables 6 and 7 was performed using the same methods used for the original genotyping, as described herein. A MassARRAY™ system (Sequenom, Inc.) was utilized to perform SNP genotyping in a high-throughput fashion. This genotyping platform was complemented by a homogeneous, single-tube assay method (hME™ or homogeneous MassEXTEND™ (Sequenom, Inc.)) in which two genotyping primers anneal to and amplify a genomic

target surrounding a polymorphic site of interest. A third primer (the MassEXTEND™ primer), which is complementary to the amplified target up to but not including the polymorphism, was then enzymatically extended one or a few bases through the polymorphic site and then terminated.

[0219] For each polymorphism, SpectroDESIGNER™ software (Sequenom, Inc.) was used to generate a set of PCR primers and a MassEXTEND™ primer which were used to genotype the polymorphism. Other primer design software could be used or one of ordinary skill in the art could manually design primers based on his or her knowledge of the relevant factors and considerations in designing such primers. Table 3 shows PCR primers and Table 4 shows extension probes used for analyzing (*e.g.*, genotyping) polymorphisms in the replication cohorts. The initial PCR amplification reaction was performed in a 5 µl total volume containing 1X PCR buffer with 1.5 mM MgCl₂ (Qiagen), 200 µM each of dATP, dGTP, dCTP, dTTP (Gibco-BRL), 2.5 ng of genomic DNA, 0.1 units of HotStar DNA polymerase (Qiagen), and 200 nM each of forward and reverse PCR primers specific for the polymorphic region of interest.

[0220] Samples were incubated at 95°C for 15 minutes, followed by 45 cycles of 95°C for 20 seconds, 56°C for 30 seconds, and 72°C for 1 minute, finishing with a 3 minute final extension at 72°C. Following amplification, shrimp alkaline phosphatase (SAP) (0.3 units in a 2 µl volume) (Amersham Pharmacia) was added to each reaction (total reaction volume was 7 µl) to remove any residual dNTPs that were not consumed in the PCR step. Samples were incubated for 20 minutes at 37°C, followed by 5 minutes at 85°C to denature the SAP.

[0221] Once the SAP reaction was complete, a primer extension reaction was initiated by adding a polymorphism-specific MassEXTEND™ primer cocktail to each sample. Each MassEXTEND™ cocktail included a specific combination of dideoxynucleotides (ddNTPs) and deoxynucleotides (dNTPs) used to distinguish polymorphic alleles from one another. Methods for verifying, allelotyping and genotyping SNPs are disclosed, for example, in U.S. Pat. No. 6,258,538, the content of which is hereby incorporated by reference. In Table 7, ddNTPs are shown and the fourth nucleotide not shown is the dNTP.

[0222] The MassEXTEND™ reaction was performed in a total volume of 9 µl, with the addition of 1X ThermoSequenase buffer, 0.576 units of ThermoSequenase (Amersham Pharmacia), 600 nM MassEXTEND™ primer, 2 mM of ddATP and/or ddCTP and/or ddGTP and/or ddTTP, and 2 mM of dATP or dCTP or dGTP or dTTP. The deoxy nucleotide (dNTP) used in the assay normally was complementary to the nucleotide at the polymorphic site in the amplicon. Samples were incubated at 94°C for 2 minutes, followed by 55 cycles of 5 seconds at 94°C, 5 seconds at 52°C, and 5 seconds at 72°C.

[0223] Following incubation, samples were desalted by adding 16 µl of water (total reaction volume was 25 µl), 3 mg of SpectroCLEAN™ sample cleaning beads (Sequenom, Inc.) and allowed to incubate for 3 minutes with rotation. Samples were then robotically dispensed using a piezoelectric dispensing device (SpectroJET™ (Sequenom, Inc.)) onto either 96-spot or 384-spot silicon chips containing a matrix that crystallized each sample (SpectroCHIP™ (Sequenom, Inc.)). Subsequently, MALDI-TOF mass spectrometry (Biflex and Autoflex MALDI-TOF mass spectrometers (Bruker Daltonics) can be used) and SpectroTYPER RT™ software (Sequenom, Inc.) were used to analyze and interpret the SNP genotype for each sample.

Genetic Analysis

[0224] Genotyping results for replication cohorts #1 and #2 are provided in Tables 8 and 9, respectively.

TABLE 8

rsID	Replication #1 (Mixed Male/Female cases and Female controls)				Meta-analysis Disc. + Rep #1
	AF OA Con	AF OA Cas	Delta	P-value	P-value
rs552	0.87	0.85	0.02	0.344	0.0300
rs12904	0.57	0.57	0.00	0.936	0.2700
rs2282146	0.08	0.1	-0.02	0.342	0.0190
rs734784	0.52	0.54	-0.02	0.451	0.7200
rs1042164	0.79	0.82	-0.03	0.161	0.9100
rs749670	0.62	0.66	-0.04	0.173	0.0019
rs955592	0.93	0.94	-0.01	0.521	0.0600
rs1143016	0.93	0.93	0.00	0.869	NA
rs755248	0.9	0.89	0.01	0.544	0.1600
rs1055055	0.64	0.64	0.00	0.947	0.3300
rs835409	0.34	0.35	-0.01	0.715	0.1300
rs927663	0.64	0.65	-0.01	0.611	0.0690
rs831038	0.35	0.37	-0.02	0.399	NA
rs33079	0.14	0.14	0.00	0.995	0.3100
rs1710880	0.66	0.62	0.04	0.087	0.9000
rs799570	0.29	0.29	0.00	0.903	0.2500
rs1282730	0.88	0.87	0.01	0.751	0.4800
rs1568694	0.93	0.94	0.00	0.928	0.2600
rs905042	0.21	0.2	0.01	0.829	0.2200
rs1957723	0.13	0.16	-0.03	0.124	0.0009
rs794018	0.74	0.72	0.02	0.518	0.0710
rs707723	0.18	0.19	-0.01	0.658	0.0650
rs1914903	0.15	0.14	0.01	0.605	0.5500
rs2062232	0.91	0.91	0.00	0.788	0.2100
rs26609	0.16	0.19	-0.02	0.226	0.0032

rsID	Replication #1 (Mixed Male/Female cases and Female controls)				Meta-analysis Disc. + Rep #1
	AF OA Con	AF OA Cas	Delta	P-value	P-value
rs1370987	0.63	0.63	-0.01	0.857	0.3900
rs1012414	0.12	0.13	-0.01	0.669	0.5600
rs435903	0.27	0.27	0.00	0.950	0.2800
rs1248	0.36	0.36	0.00	0.917	0.2400
rs703508	0.11	0.12	-0.01	0.558	0.0660
rs226465	0.87	0.88	-0.01	0.436	0.0500
rs241448	0.74	0.75	-0.01	0.805	0.4100
rs763155	0.86	0.88	-0.02	0.273	0.8800
rs1040461	0.92	0.92	0.00	0.826	NA
rs1022646	0.85	0.87	-0.02	0.219	0.8200
rs1569112	0.16	0.18	-0.02	0.402	0.8800
rs805623	0.87	0.88	-0.01	0.460	0.0370
rs1019850	0.69	0.7	0.00	0.890	0.3700
AA	0.47	0.48	-0.01	0.681	0.1200
rs279941	0.87	0.89	-0.01	0.400	0.0340
rs1062230	0.26	0.26	0.00	0.896	0.4200
rs1859911	0.71	0.75	-0.04	0.128	0.9000
rs1477261	0.16	0.16	0.00	0.986	0.3000
rs1191119	0.89	0.88	0.01	0.569	0.1200
rs1393890	0.29	0.31	-0.02	0.527	0.1400
rs1478714	0.69	0.67	0.03	0.300	0.0140
rs868213	0.92	0.93	-0.01	0.455	0.7000
rs690115	0.2	0.21	-0.01	0.729	0.4900
rs1465501	0.11	0.1	0.01	0.718	0.5600
rs899173	0.1	0.11	0.00	0.924	0.3300
rs10477	0.89	0.88	0.01	0.691	0.4700
rs926393	0.3	0.31	-0.01	0.830	0.4200
rs465271	0.86	0.85	0.01	0.516	0.0660
rs13847	0.86	0.85	0.01	0.547	0.5900
rs738658	0.14	0.15	-0.01	0.536	0.6700

TABLE 9

rsID	Replication #2 (Newfoundland) (Male/Female cases and controls)				Meta-analysis Disc. + Rep #2
	AF OA Con	AF OA Cas	Delta	P-value	Not Done
rs552	0.85	0.86	-0.014	0.496	
rs12904	0.58	0.57	0.011	0.719	
rs2282146	0.08	0.08	0.002	0.876	
rs734784	0.53	0.54	-0.003	0.907	
rs1042164	0.83	0.80	0.026	0.248	
rs749670	0.66	0.62	0.036	0.208	
rs955592	0.95	0.92	0.033	0.027	

rsID	Replication #2 (Newfoundland) (Male/Female cases and controls)				Meta-analysis
	AF OA Con	AF OA Cas	Delta	P-value	Disc. + Rep #2 Not Done
rs1143016	0.96	0.94	0.015	0.236	
rs755248	0.89	0.90	-0.009	0.608	
rs1055055	0.64	0.61	0.034	0.249	
rs835409	0.36	0.31	0.047	0.101	
rs927663	0.67	0.68	-0.013	0.631	
rs831038	0.34	0.35	-0.014	0.612	
rs33079	0.17	0.19	-0.019	0.417	
rs1710880	0.64	0.62	0.029	0.309	
rs799570	0.35	0.30	0.058	0.033	
rs1282730	0.89	0.89	-0.001	0.982	
rs1568694	0.95	0.94	0.009	0.518	
rs905042	0.19	0.20	-0.002	0.933	
rs1957723	0.18	0.20	-0.017	0.454	
rs794018	0.73	0.72	0.015	0.586	
rs707723	0.20	0.21	-0.007	0.759	
rs1914903	0.14	0.16	-0.022	0.285	
rs2062232	0.92	0.91	0.008	0.632	
rs26609	0.19	0.18	0.005	0.827	
rs1370987	0.59	0.61	-0.023	0.423	
rs1012414	0.15	0.14	0.008	0.679	
rs435903	0.24	0.26	-0.026	0.316	
rs1248	0.33	0.38	-0.051	0.078	
rs703508	0.10	0.11	-0.002	0.916	
rs226465	0.89	0.89	-0.007	0.699	
rs241448	0.76	0.77	-0.007	0.778	
rs763155	0.89	0.84	0.049	0.016	
rs1040461	0.91	0.91	0.001	0.948	
rs1022646	0.86	0.86	-0.001	0.974	
rs1569112	0.16	0.17	-0.016	0.446	
rs805623	0.89	0.87	0.022	0.256	
rs1019850	0.71	0.69	0.026	0.341	
AA	0.48	0.44	0.035	0.234	
rs279941	0.91	0.87	0.037	0.047	
rs1062230	0.23	0.22	0.011	0.653	
rs1859911	0.72	0.71	0.015	0.560	
rs1477261	0.17	0.14	0.031	0.143	
rs1191119	0.86	0.88	-0.017	0.377	
rs1393890	0.30	0.28	0.017	0.516	
rs1478714	0.68	0.70	-0.025	0.358	
rs868213	0.91	0.93	-0.019	0.260	
rs690115	0.19	0.18	0.005	0.811	
rs1465501	0.10	0.12	-0.020	0.282	
rs899173	0.14	0.12	0.020	0.319	
rs10477	0.86	0.88	-0.016	0.442	
rs926393	0.37	0.32	0.042	0.137	

rsID	Replication #2 (Newfoundland) (Male/Female cases and controls)				Meta-analysis Disc. + Rep #2 Not Done
	AF OA Con	AF OA Cas	Delta	P-value	
rs465271	0.87	0.85	0.023	0.263	
rs13847	0.84	0.85	-0.012	0.582	
rs738658	0.18	0.15	0.021	0.340	

[0225] To combine the evidence for association from multiple sample collections, a meta-analysis procedure was employed. The allele frequencies were compared between cases and controls within the discovery sample, as well as within the replication cohort #1 using the DerSimonian-Laird approach (DerSimonian, R. and N. Laird. 1986. Meta-analysis in clinical trials. Control Clin Trials 7: 177-188.)

[0226] The absence of a statistically significant association in one or more of the replication cohorts should not be interpreted as minimizing the value of the original finding. There are many reasons why a biologically derived association identified in a sample from one population would not replicate in a sample from another population. The most important reason is differences in population history. Due to bottlenecks and founder effects, there may be common disease predisposing alleles present in one population that are relatively rare in another, leading to a lack of association in the candidate region. Also, because common diseases such as arthritis-related disorders are the result of susceptibilities in many genes and many environmental risk factors, differences in population-specific genetic and environmental backgrounds could mask the effects of a biologically relevant allele. For these and other reasons, statistically strong results in the original, discovery sample that did not replicate in one or more of the replication samples may be further evaluated in additional replication cohorts and experimental systems.

Example 4

KIAA0296 Region Proximal SNPs

[0227] SNP rs749670 is associated with osteoarthritis and is described in Table A. It lies within the KIAA0296 gene and codes for a G327E amino acid change. The thymine allele of SNP rs749670 is associated with osteoarthritis (see Table 5) and codes for glutamic acid. KIAA0296 shares homology with C2H2-type Zn-finger protein and is likely a novel transcription factor. One-hundred one additional allelic variants proximal to rs749670 were identified and subsequently allelotyped in osteoarthritis case and control sample sets as described in Examples 1 and 2. The polymorphic variants are set forth in Table 10. The chromosome positions provided in column four of Table 10 are based on Genome “Build 34” of NCBI’s GenBank.

TABLE 10

dbSNP rs#	Chromosome	Position in SEQ ID NO: 1	Chromosome Position	Allele Variants
rs7500176	16	247	31077197	a/g
rs6565212	16	1535	31078485	c/t
rs8054046	16	2386	31079336	c/t
rs8056842	16	6440	31083390	c/t
rs732173	16	9133	31086083	g/t
rs732172	16	9143	31086093	a/g
rs7188557	16	9471	31086421	a/t
rs2288004	16	13150	31090100	c/g
rs4337310	16	13717	31090667	c/t
rs2016554	16	14466	31091416	a/g
rs6565213	16	15769	31092719	a/c
rs7204762	16	16870	31093820	a/g
rs4889529	16	18545	31095495	c/t
rs6565214	16	18749	31095699	c/t
rs7499674	16	19123	31096073	g/t
rs6565215	16	20736	31097686	a/g
rs1023623	16	21038	31097988	c/t
rs1023624	16	21046	31097996	c/t
rs1023625	16	21050	31098000	c/t
rs1549297	16	21056	31098006	a/t
rs3084894	16	21706	31098656	-/acc
rs8048228	16	23170	31100120	a/g
rs7405432	16	25028	31101978	a/t
rs8054249	16	27871	31104821	a/g
rs8061047	16	28070	31105020	c/t
rs7187220	16	31717	31108667	a/g
rs8046978	16	32019	31108969	a/g
rs2288003	16	32318	31109268	a/g
rs7196421	16	33080	31110030	a/g
rs7196431	16	33101	31110051	a/g
rs7203158	16	34236	31111186	a/g
rs2303223	16	34285	31111235	c/t
rs2032917	16	34818	31111768	c/g
rs8044134	16	35168	31112118	c/g
rs4889531	16	37981	31114931	c/t
rs4889532	16	38113	31115063	c/g
rs4889533	16	38117	31115067	c/t
rs881929	16	38481	31115431	g/t
rs8047104	16	38615	31115565	c/g
rs8047803	16	38944	31115894	a/c
rs4644874	16	39288	31116238	a/c
rs2359673	16	41385	31118335	c/t
rs4435271	16	42136	31119086	a/t
rs7197717	16	42185	31119135	a/c
rs2359674	16	42353	31119303	a/g
rs6565217	16	42434	31119384	a/g

dbSNP rs#	Chromosome	Position in SEQ ID NO: 1	Chromosome Position	Allele Variants
rs2303222	16	44580	31121530	a/g
rs4889615	16	44675	31121625	a/t
rs4624197	16	45739	31122689	g/t
rs3751853	16	46439	31123389	c/t
rs749671	16	47457	31124407	c/t
rs749670	16	47735	31124685	c/t
rs3751855	16	50319	31127269	c/t
rs3751856	16	50708	31127658	a/g
rs7196726	16	51185	31128135	a/g
rs889550	16	53002	31129952	a/g
rs750952	16	53064	31130014	c/t
rs2077633	16	53637	31130587	a/g
rs7199949	16	55274	31132224	c/g
rs2032916	16	55825	31132775	c/t
rs4468641	16	55986	31132936	a/c
rs4889535	16	56684	31133634	c/g
rs4316775	16	57653	31134603	c/t
rs4313819	16	57659	31134609	c/g
rs6565218	16	57692	31134642	g/t
rs4318224	16	57775	31134725	c/t
rs1046030	16	61313	31138263	c/t
rs7294	16	61431	31138381	a/g
rs7200749	16	61699	31138649	a/g
rs2359612	16	62906	31139856	a/g
rs8050894	16	63619	31140569	c/g
rs2884737	16	64664	31141614	a/c
rs1895514	16	68452	31145402	g/t
rs8060209	16	69665	31146615	c/t
rs8060217	16	69681	31146631	c/t
rs7196161	16	70091	31147041	a/g
rs8062336	16	74637	31151587	a/g
rs8043778	16	74760	31151710	a/g
rs2032915	16	76523	31153473	a/g
rs4889616	16	78559	31155509	c/g
rs1045564	16	79549	31156499	a/c
rs2303221	16	79882	31156832	c/t
rs1549296	16	81339	31158289	a/g
rs889555	16	81681	31158631	c/t
rs5816521	16	81696	31158646	-/g
rs749767	16	83517	31160467	c/t
rs2884738	16	85431	31162381	a/c
rs2052581	16	86332	31163282	c/t
rs4889617	16	87358	31164308	a/g
rs4889619	16	87725	31164675	c/t
rs1978487	16	89052	31166002	a/g
rs1978486	16	90020	31166970	a/g
rs1978485	16	90231	31167181	a/g

dbSNP rs#	Chromosome	Position in SEQ ID NO: 1	Chromosome Position	Allele Variants
rs4889620	16	90284	31167234	a/g
rs4889621	16	90447	31167397	c/t
rs3214477	16	90601	31167551	-/g
rs4527034	16	90724	31167674	a/g
rs1060506	16	92559	31169509	c/t
rs7200125	16	95176	31172126	a/g
rs6565219	16	95195	31172145	c/t
rs889548	16	96822	31173772	a/g

Assay for Verifying and Allelotyping SNPs

[0228] The methods used to verify and allelotype the 101 proximal SNPs of Table 10 are the same methods described in Examples 1 and 2 herein. The primers and probes used in these assays are provided in Table 11 and Table 12, respectively.

TABLE 11

dbSNP rs#	Forward PCR primer	Reverse PCR primer
rs7500176	ACGTTGGATGACAGTGGCTCATGCCTGTAA	ACGTTGGATGTTTCACCATATTGGCCAGGC
rs6565212	ACGTTGGATGTTAGGAAGGATGTGGAAGGG	ACGTTGGATGGACCTGACCTCAAAGAGAAG
rs8054046	ACGTTGGATGCACTGAAGTTTAGAGCAGCC	ACGTTGGATGTGCACAGTGGGTAACTGTAG
rs8056842	ACGTTGGATGATGAGGTTTCACCTTGTTGG	ACGTTGGATGATCATAGCACTTTGCGAGGC
rs732173	ACGTTGGATGAGACCAGGCTCAGTCCAAAC	ACGTTGGATGTGGCCAAACCTGGAAGACAC
rs732172	ACGTTGGATGCTCAGTCCAAACTGCCAGAC	ACGTTGGATGCATGGCCAAACCTGGAAGAC
rs7188557	ACGTTGGATGAACATCTGTACAAGGCTGGG	ACGTTGGATGATTGGCTGTAGCATGACTGA
rs2288004	ACGTTGGATGAAAGACACTGGAAGGCTGTG	ACGTTGGATGAGAGAAGGTGGAGCTCTTTC
rs4337310	ACGTTGGATGAGGGAAGAGATGTACACAGG	ACGTTGGATGTTTGGAGCAGATCTGGTAGG
rs2016554	ACGTTGGATGAAGCAATCCTCCCACCTCAG	ACGTTGGATGCAAGAGCAAACTCCCTCTC
rs6565213	ACGTTGGATGAGATGGAGTCTCACTCCATC	ACGTTGGATGTGAGGCAGGAGAATCGCTTG
rs7204762	ACGTTGGATGAGTGGCTCACACCTGTAATC	ACGTTGGATGGCTGGTCTTGAACCTCTGAC
rs4889529	ACGTTGGATGCAAGCAATCCTTGCTCAAG	ACGTTGGATGGGTGGTTCACATCTGCAATC
rs6565214	ACGTTGGATGTGATCTCGGCTCACTGCAAG	ACGTTGGATGAAAATTAGCCGGGCATGGTG
rs7499674	ACGTTGGATGAACTAGGGAACCTTCCCAC	ACGTTGGATGTGGGCCCCACTAAGTCTAAA
rs6565215	ACGTTGGATGAGACGGAAGTTCCAGCTTG	ACGTTGGATGTGGGACCACTCTGTTCTATG
rs1023623	ACGTTGGATGACAGAGCAAGACTCCATCTC	ACGTTGGATGTCCTCTTCAGAGCTGTTAC
rs1023624	ACGTTGGATGTGACAGAGCAAGACTCCATC	ACGTTGGATGGTCTTAACCACTGAGCCTAT
rs1023625	ACGTTGGATGTGGTGACAGAGCAAGACTCC	ACGTTGGATGTCAGGTCCTAACCAGTGAGC
rs1549297	ACGTTGGATGTTGCATTGATCCGAGATCGC	ACGTTGGATGTCAGGTCCTAACCAGTGAGC
rs3084894	ACGTTGGATGTCCCAGGTTCAAGCGATTCT	ACGTTGGATGCCATGAAACCCCATCTCTAC
rs8048228	ACGTTGGATGAATTGCTTGAACCTGGGAGG	ACGTTGGATGTTGACAGTCTCCCTCTATC
rs7405432	ACGTTGGATGAGATCATGCCACTGCACTAC	ACGTTGGATGCACTGCACTTGGCCTAATTG
rs8054249	ACGTTGGATGATCTCCTGACCTCATGATCT	ACGTTGGATGTAATCAAACACCAGGCTGGG
rs8061047	ACGTTGGATGATGATCACAGCTCACTGCAG	ACGTTGGATGCTCCCTGCCTCTACAAAAAG
rs7187220	ACGTTGGATGAAGGAGACCTTCTCCACAAT	ACGTTGGATGCCGGTCAGAGAAGCTCTTGC

dbSNP rs#	Forward PCR primer	Reverse PCR primer
rs8046978	ACGTTGGATGTGCACAGGAGCTGGTGGTG	ACGTTGGATGATCACACCACCTGACTCCGG
rs2288003	ACGTTGGATGACCGGCCGTTCAAGTGCCTG	ACGTTGGATGAGAGTGCACCAGCGCGTGC
rs7196421	ACGTTGGATGTTACGCCATTCTCCTGCCT	ACGTTGGATGAAATTAGCCAGGCGTGGTGG
rs7196431	ACGTTGGATGAGATCTCGGCTCACTGCAAG	ACGTTGGATGATGTAGTCCCAGCTACTCGG
rs7203158	ACGTTGGATGAAGCCTATGCGGAGCTCAAG	ACGTTGGATGATTGGCTGCAGCAACGCTGT
rs2303223	ACGTTGGATGACCCTCACCGCTCATGGTTG	ACGTTGGATGTGCGGCCCTACAGCTGTGA
rs2032917	ACGTTGGATGCCTGGGCGCGTTTGAAATG	ACGTTGGATGAGCCCCGGCTACAAGCGCT
rs8044134	ACGTTGGATGACTAAGAAAGGAGGCTGAGG	ACGTTGGATGACAGTGTTTGGAAAAGCCCG
rs4889531	ACGTTGGATGATTCTCACCCTCACTCTGTC	ACGTTGGATGGACCGTGTGTAATGTACTGC
rs4889532	ACGTTGGATGGGGACAAGAATCCCTATCTC	ACGTTGGATGTAGAGCCAGACACATTGCTG
rs4889533	ACGTTGGATGCTCTGTAAAGTAGGGACAAG	ACGTTGGATGTAGAGCCAGACACATTGCTG
rs881929	ACGTTGGATGTTGACCCAGTGTTCTGAGC	ACGTTGGATGCCAGCTACCTGGTGTCTAAC
rs8047104	ACGTTGGATGGTGGGATGTTAGACAGAGAC	ACGTTGGATGTGCCAGGTTGGTCTCAGCAT
rs8047803	ACGTTGGATGAAAGTGCTGGGATTACAGGC	ACGTTGGATGAAATACAGATTCTGAGGCC
rs4644874	ACGTTGGATGAGTCTTGCTATGTTGCCTGG	ACGTTGGATGTAATCCAGCACTTTGGGAG
rs2359673	ACGTTGGATGGTGTGATGTCAGTTCACTGC	ACGTTGGATGATCCCAAATACTTGGGAGGC
rs4435271	ACGTTGGATGACAGTGGTCTCAAGAACTCC	ACGTTGGATGTGGCTCATGCCTGTAATCAC
rs7197717	ACGTTGGATGTGTGATTACAGGCATGAGCC	ACGTTGGATGGCTTGCAAGGAGTATTGTCC
rs2359674	ACGTTGGATGGCCTAGCAGTTCATTATGAG	ACGTTGGATGCCTTGCTCCAAATACAGTC
rs6565217	ACGTTGGATGAAGAACGCTAATCCTACTGG	ACGTTGGATGTGGAGACAAGGCCCTTATGG
rs2303222	ACGTTGGATGTTGGGAAAAGTCCTCCAGAG	ACGTTGGATGGCGCAGAAAGGGAGAAAAAG
rs4889615	ACGTTGGATGTAAGTTCTAGGTCTGCACGG	ACGTTGGATGATGCACCGGAACGATTCTAG
rs4624197	ACGTTGGATGCGCTAAGAGAGTCTTTTGGG	ACGTTGGATGCAGAGCCGAGACTCCATCTCA
rs3751853	ACGTTGGATGTCCCCTAGGCTTAAGTCATC	ACGTTGGATGGGTCTGTGATCAGAAGTAGG
rs749671	ACGTTGGATGTGACTACATTTGTACCGCCG	ACGTTGGATGTCAGTAGTGAACCTTCACAGG
rs749670	ACGTTGGATGTCTCATCTGTGTGCCCATTG	ACGTTGGATGATGAGGGTGAAAGGCAGGAG
rs3751855	ACGTTGGATGAAGAAGAGGTGTGGGAGGAG	ACGTTGGATGTCAGAGCTGGCTTCAGTCTG
rs3751856	ACGTTGGATGAGCTGTACTGGCCCGTCTCG	ACGTTGGATGCAGTGCGGGCGGACCTATC
rs7196726	ACGTTGGATGGACCTAGTTAGGAAGTGAAG	ACGTTGGATGTCAGGGCAGCAAGCTCAGAAG
rs889550	ACGTTGGATGTCCACCCAGCACTGCTGGA	ACGTTGGATGCAGGTCTCTGCTGAGGGAAC
rs750952	ACGTTGGATGTTCCCTCAGCAGGACCTGG	ACGTTGGATGGGTGGCCACTAGATGGAATG
rs2077633	ACGTTGGATGTTTCTCAGGAGTAGTTCGGG	ACGTTGGATGAAAGAAGCCAGATCTGGGTC
rs7199949	ACGTTGGATGTCCCCTCAGGCAGGTGGT	ACGTTGGATGCAGCCTGTGACACTGGGAG
rs2032916	ACGTTGGATGGTTCCCCTCATTACTGAAGG	ACGTTGGATGTGCCACTTGCTGTAGTTAC
rs4468641	ACGTTGGATGATGAGTCAGGAATACGGGAG	ACGTTGGATGAATGCCCTACTTGTCACCTC
rs4889535	ACGTTGGATGCTATGGCAGACACCTCTGA	ACGTTGGATGGAAGAGAAGGAGCAGAAAGG
rs4316775	ACGTTGGATGAGTAGCTCACGCTTGTAATC	ACGTTGGATGCTATGTTGCACAGGCTAGTC
rs4313819	ACGTTGGATGTGCACAGGCTAGTCTTGAAC	ACGTTGGATGAGTAGCTCACGCTTGTAATC
rs6565218	ACGTTGGATGTTAAAGTCACAGACTGAGGC	ACGTTGGATGTTGAACTCTTGGGCTCAAGC
rs4318224	ACGTTGGATGTCAGTCTGTGACTTTAAGCG	ACGTTGGATGACCACCTTTCATGGTAGAAG
rs1046030	ACGTTGGATGGTCTCCAAAGCTCTTCCATT	ACGTTGGATGGATTGATCTAAGAACTTTA
rs7294	ACGTTGGATGGCACTGGGTGTAAAAAGAG	ACGTTGGATGTTCTAGATTACCCCTCCTC
rs7200749	ACGTTGGATGGAGCACGAAGAAGGATCC	ACGTTGGATGTCTGTCTGATGCTGCTGAG
rs2359612	ACGTTGGATGAAATCGGCCAAGTCTGAACC	ACGTTGGATGTCCAGAGAAGGCATCACTGA
rs8050894	ACGTTGGATGAATCTTGGTGATCCACACAG	ACGTTGGATGTAGTTACCTCCCCACATCCC
rs2884737	ACGTTGGATGTCATTATGCTAACGCCTGGC	ACGTTGGATGTTGACGATGGTCTCAAGGAC
rs1895514	ACGTTGGATGCAATCTCAGCTCACTGCAAC	ACGTTGGATGTAATCCAGCTACTTGGGAG

dbSNP rs#	Forward PCR primer	Reverse PCR primer
rs8060209	ACGTTGGATGGGTCAGGAGTTTAAGACAAG	ACGTTGGATGCCATGCCCGGCTAATTTTTG
rs8060217	ACGTTGGATGTGAGTAGCTGGGATTACAGG	ACGTTGGATGAGACAAGCTTGGCCAACATG
rs7196161	ACGTTGGATGGTGTGTTTTAGTAGAGACGGG	ACGTTGGATGATCCACGCACTTTAGGAAGC
rs8062336	ACGTTGGATGTGCTCCCCACATCTCAGACG	ACGTTGGATGAAGCGAGGAGCGCCTCTTC
rs8043778	ACGTTGGATGTTCTCCTCATTCTCAGACGGG	ACGTTGGATGATCGTCTGAGATGTGGGGAG
rs2032915	ACGTTGGATGATTCCCACCCGTTCTTTCCC	ACGTTGGATGTTCCCGCTCCCTTTTACCAC
rs4889616	ACGTTGGATGGAACCAAGAAGTGAAGGAG	ACGTTGGATGTGTAAAGCGCACAGATCACG
rs1045564	ACGTTGGATGTGTCAGCATCCTCGACGCAC	ACGTTGGATGACCCAGGCGACCCAAAATGG
rs2303221	ACGTTGGATGAGAACCCCCAACACTCTCCC	ACGTTGGATGAGCGGAGAAGGTGCGCAAG
rs1549296	ACGTTGGATGATGCTGCTGAACCTCCTAAC	ACGTTGGATGAGCAGGGTTTCTCAACCATG
rs889555	ACGTTGGATGAGACCAGTAGGTACAAGCAC	ACGTTGGATGTCAAGAATGCCATGAGGTGG
rs5816521	ACGTTGGATGATTGTGGCTCTATGCAGAGG	ACGTTGGATGTCAAGAATGCCATGAGGTGG
rs749767	ACGTTGGATGCTGATAGAAAGGACCAAGGA	ACGTTGGATGCTGGAGTTCTGATTCAAGTC
rs2884738	ACGTTGGATGAGAAGTCTTGAACCCAGGA	ACGTTGGATGATGGAGTCTTGTGTGTCGG
rs2052581	ACGTTGGATGTGGGACATGCGGATATGGAG	ACGTTGGATGGAGGGTTCTGTGAGAGTCAG
rs4889617	ACGTTGGATGCAGAGCGAGACTCCATCTCA	ACGTTGGATGACACTCGCGCTGGCCTAATG
rs4889619	ACGTTGGATGAAAATTAGATGGGCGTGGTG	ACGTTGGATGATCTCGGCTCACTGCAACCT
rs1978487	ACGTTGGATGTCCCTTCTCTATGTTCTGTC	ACGTTGGATGATGGAGGAAGACAGAGAGAG
rs1978486	ACGTTGGATGTACCTAGGGTCACAGATTTG	ACGTTGGATGGGGTATGTGGTAAAATGAGC
rs1978485	ACGTTGGATGTCAAGCAATTTTCTGCCTC	ACGTTGGATGCCATCTGTACCAAAAAGACG
rs4889620	ACGTTGGATGTGGCAAACCCCATCTGTAC	ACGTTGGATGAGTAGTTGGGATTACAGGTG
rs4889621	ACGTTGGATGTACTCAATCACTGCCACAAC	ACGTTGGATGGCCAGTTATTTTCTCATTTCG
rs3214477	ACGTTGGATGACTCGAGACTGGATCACTTC	ACGTTGGATGCCTTTTGTTCAGCCTTACC
rs4527034	ACGTTGGATGAAGTATGGGCCATAAGAGTG	ACGTTGGATGTATGTACACTACGTGGGCTG
rs1060506	ACGTTGGATGATCAGGAGTGCAAACCCAGAG	ACGTTGGATGGGATGAAGCTGCAATAGCTG
rs7200125	ACGTTGGATGATTTTGCCATTGCACTCCAG	ACGTTGGATGTACAGGCATGAGCCATAGCC
rs6565219	ACGTTGGATGCTTGGCCTCTCAAAGTGCTG	ACGTTGGATGAGGGCGAGGCTCCATTTCAA
rs889548	ACGTTGGATGCTGGCCAAGTCCTAATACAG	ACGTTGGATGCCCAATTCCAGAGATGTCAG

TABLE 12

dbSNP rs#	Extend Primer	Term Mix
rs7500176	GATCACGAGGTCAGGAGTTC	ACT
rs6565212	GCTGGAAAAGTGTGAGGGT	ACT
rs8054046	TTTAGAGCAGCCGATACCCA	ACG
rs8056842	GCTGGTCTCGAACTCCTGA	ACG
rs732173	GCTCAGTCCAACTGCCAG	CGT
rs732172	ACTGCCAGACTCCCGCCA	ACG
rs7188557	CCTGGCCCTGGTTGTGAGT	CGT
rs2288004	CGGCAGATCCAGTGTGTC	ACT
rs4337310	CACGGAATCTCCAGTGCAC	ACT
rs2016554	GGCACGTACCACTGACATG	ACG
rs6565213	GCAGTGGCGCAATCTTGAC	ACT
rs7204762	CCCAGCACTTTGGGAGGC	ACG

dbSNP rs#	Extend Primer	Term Mix
rs4889529	CTCAAGTGATCCTCCTGCCT	ACG
rs6565214	GAGTAGCTGGGACTACAGG	ACG
rs7499674	GTTCTTCTCAACATCTGCCCA	ACT
rs6565215	TTTCCTTCAGACAGGGCTCT	ACT
rs1023623	GACTCCATCTCAAAAAAAAAAAAAA	ACT
rs1023624	GAGCAAGACTCCATCTCAAAAA	ACT
rs1023625	CAGAGCAAGACTCCATCTCA	ACT
rs1549297	GGTGACAGAGCAAGACTCC	CGT
rs3084894	CGAGTAGGTGGGACTACAG	ACT
rs8048228	TGAGCCGAGATGGCAACAC	ACG
rs7405432	CTACAGGCTAGGAGACAGAG	CGT
rs8054249	AAAGTGCTGGGATTACAGGC	ACT
rs8061047	CCTCCTGAGGAGCTGGTCT	ACT
rs7187220	GGCCCTTCCCCTGCACC	ACG
rs8046978	AGAGTTCAGCCGCCCGG	ACG
rs2288003	GTGACAAGACGTTCTGTGGC	ACT
rs7196421	CTCAGCCTCCCGAGTAGC	ACG
rs7196431	CGGGTTCACGCCATTCTCC	ACG
rs7203158	CAACCATGAGCGGTGAGGG	ACG
rs2303223	TTGAGCTCCGCATAGGCTTT	ACT
rs2032917	TGGAAATGTCTTGGTACAGGACA	ACT
rs8044134	CCTACACGTCCCCCCCC	ACT
rs4889531	CAACTCTGTCAGGTAAGTACT	ACT
rs4889532	CAAGAATCCCTATCTCAGAAAG	ACT
rs4889533	GGACAAGAATCCCTATCTCAG	ACT
rs881929	CTGCCTCTTGCCAGCTCTG	ACT
rs8047104	CAGAGACCTAGCCTACCTG	ACT
rs8047803	TTACAGGCGAGAGCCACCA	CGT
rs4644874	GGGCTCAAGTGATCCTCCC	CGT
rs2359673	ACTGCGACCTCTGCCTCC	ACG
rs4435271	GCTTCAGATGCTCCTCCACT	CGT
rs7197717	GCATGAGCCGTGACCAGC	CGT
rs2359674	GAATGTTTGTGTTCCCTGTCC	ACT
rs6565217	CCAGGGCCATACCCTTATGA	ACG
rs2303222	AAAGTGTCACCAAAGTAC	ACG
rs4889615	GCGGCGTCTTTGCACGCTA	CGT
rs4624197	AGAGAGTCTTTTGGGGTTTTTT	ACT
rs3751853	CCTACAGGTATAGCTAAGGAA	ACT
rs749671	ATTTGTACCGCCGCTCCTC	ACG
rs749670	GGTGGTGGGCATCCCTTTC	ACG
rs3751855	AGAGCCCAGGCTGGAGAC	ACG
rs3751856	CCGTCTCGTGGCTGCGC	ACG
rs7196726	GTTAGGAACTGAGGAACCCAG	ACG
rs889550	AGCACTGCTGGAAGCCGC	ACT

dbSNP rs#	Extend Primer	Term Mix
rs750952	GCTGGCCTCTCCACCTCC	ACG
rs2077633	CCATATCTTCTCCTCTCCCC	ACG
rs7199949	CAGGCAGGTGGTGGTCAG	ACT
rs2032916	CCAAAGTTCCAGAGAGGTTAA	ACT
rs4468641	ATACGGGAGGCAGGCCCA	ACT
rs4889535	CAGACACCCTCTGATTGCAG	ACT
rs4316775	GAGGATCGCTTGAGCCCAA	ACT
rs4313819	GCTAGTCTTGAACCTTTGGG	ACT
rs6565218	CTCACGCTTGTAAATCCCAGC	CGT
rs4318224	TTCCCTTGCAACCTGAGTTTT	ACG
rs1046030	GCCCAGGGAGGGAAGGTT	ACG
rs7294	TTGGTCCATTGTCATGTG	ACG
rs7200749	GAAGAACAGGATCCAGGCCA	ACT
rs2359612	CCATGTGTCTAGCCAGGACC	ACT
rs8050894	CCAGCTAGCTGCTCATCAC	ACT
rs2884737	TCGCCAACACCCCCCTTC	CGT
rs1895514	CCCCTCTCGGGTTCAAGC	CGT
rs8060209	TGGCCAACATGGCGAAACC	ACG
rs8060217	CCATGCCCGGCTAATTTTTGT	ACT
rs7196161	AACTCCTGACCTCATGATCC	ACT
rs8062336	TCACTTCCTAGATGGGAAGG	ACG
rs8043778	CGCTCCTCACCTCCCAGA	ACG
rs2032915	TTCTTTCCCAACGTCCTGGA	ACT
rs4889616	GAAGTGAAGGAGGACAAGA	ACT
rs1045564	GTCCCTGAAGTCGGAGAAG	CGT
rs2303221	CTCTCCCTCCCGCCTACAT	ACG
rs1549296	TGCACGGGGCAGCCCCT	ACT
rs889555	AGCACCCCGGTTCTGTCC	ACT
rs5816521	CCAGTAGGTACAAGCACCC	ACT
rs749767	GACCAAGGATTTGGGCAAAG	ACT
rs2884738	CCAGGAGGTGGAGGTTGCA	ACT
rs2052581	GGATATGGAGGGCCGATTGT	ACT
rs4889617	GAGACTCCATCTCAAAAAAAAAA	ACT
rs4889619	GCAGAGGAATCGCTTGAACC	ACG
rs1978487	GTTCTGCAACATTTTTTCTTA	ACG
rs1978486	GGTACACAGATTGAAAAGTG	ACT
rs1978485	TTTTCTGCCTCAGCCTCC	ACG
rs4889620	ACCCCATCTGTACCAAAAAGA	ACG
rs4889621	CTGTGAGGTGGATCAGGTTG	ACT
rs3214477	GCAGAATCTGTGATGGAAAAAG	ACT
rs4527034	CCAGGGCAGCCAACTCCC	ACG
rs1060506	AAGTCTCCAGACACCCAGA	ACG
rs7200125	AGGCTCCATTTCAAAAAAAAAA	ACT
rs6565219	AAAGTGCTGGGATTACAGGC	ACT

dbSNP rs#	Extend Primer	Term Mix
rs889548	AGTCCTAATACAGTGGATGTC	ACT

Genetic Analysis

[0229] Allelotyping results from the discovery cohort are shown for cases and controls in Table 13. The allele frequency for the A2 allele is noted in the fifth and sixth columns for osteoarthritis case pools and control pools, respectively, where “AF” is allele frequency. The allele frequency for the A1 allele can be easily calculated by subtracting the A2 allele frequency from 1 (A1 AF = 1-A2 AF). For example, the SNP rs732173 has the following case and control allele frequencies: case A1 (G) = 0.55; case A2 (T) = 0.45; control A1 (G) = 0.58; and control A2 (T) = 0.42, where the nucleotide is provided in paranthesis. Some SNPs are labeled “untyped” because of failed assays.

TABLE 13

dbSNP rs#	Position in SEQ ID NO: 1	Chromosome Position	A1/A2 Allele	F A2 Case AF	F A2 Control AF	F p- Value
rs7500176	247	31077197	A/G			
rs6565212	1535	31078485	C/T			
rs8054046	2386	31079336	C/T			
rs8056842	6440	31083390	C/T			
rs732173	9133	31086083	G/T	0.45	0.42	0.382
rs732172	9143	31086093	A/G			
rs7188557	9471	31086421	A/T			
rs2288004	13150	31090100	C/G	0.52	0.45	0.026
rs4337310	13717	31090667	C/T	0.18	untyped	
rs2016554	14466	31091416	A/G			
rs6565213	15769	31092719	A/C			
rs7204762	16870	31093820	A/G			
rs4889529	18545	31095495	C/T			
rs6565214	18749	31095699	C/T			
rs7499674	19123	31096073	G/T			
rs6565215	20736	31097686	A/G			
rs1023623	21038	31097988	C/T	0.02	untyped	
rs1023624	21046	31097996	C/T	0.16	0.11	0.035
rs1023625	21050	31098000	C/T	0.32	NA	
rs1549297	21056	31098006	A/T			
rs3084894	21706	31098656	-/ACC			
rs8048228	23170	31100120	A/G	0.54	0.61	0.040
rs7405432	25028	31101978	A/T	0.35	0.43	0.025
rs8054249	27871	31104821	A/G			
rs8061047	28070	31105020	C/T	0.21	0.21	0.903
rs7187220	31717	31108667	A/G			
rs8046978	32019	31108969	A/G	0.34	0.28	0.083
rs2288003	32318	31109268	A/G			
rs7196421	33080	31110030	A/G			
rs7196431	33101	31110051	A/G			
rs7203158	34236	31111186	A/G			
rs2303223	34285	31111235	C/T	0.52	0.45	0.060
rs2032917	34818	31111768	C/G			

dbSNP rs#	Position in SEQ ID NO: 1	Chromosome Position	A1/A2 Allele	F A2 Case AF	F A2 Control AF	F p- Value
rs8044134	35168	31112118	C/G	0.97	0.97	0.856
rs4889531	37981	31114931	C/T			
rs4889532	38113	31115063	C/G			
rs4889533	38117	31115067	C/T			
rs881929	38481	31115431	G/T	0.38	0.34	0.228
rs8047104	38615	31115565	C/G	0.60	0.65	0.117
rs8047803	38944	31115894	A/C	0.35	0.33	0.437
rs4644874	39288	31116238	A/C			
rs2359673	41385	31118335	C/T	0.18	0.20	0.563
rs4435271	42136	31119086	A/T			
rs7197717	42185	31119135	A/C			
rs2359674	42353	31119303	A/G	0.22	0.18	0.122
rs6565217	42434	31119384	A/G	0.35	0.33	0.608
rs2303222	44580	31121530	A/G	0.60	0.52	0.022
rs4889615	44675	31121625	A/T			
rs4624197	45739	31122689	G/T			
rs3751853	46439	31123389	C/T			
rs749671	47457	31124407	C/T	0.32	0.37	0.095
rs749670	47735	31124685	C/T			
rs3751855	50319	31127269	C/T	0.53	0.57	0.287
rs3751856	50708	31127658	A/G			
rs7196726	51185	31128135	A/G	0.41	0.37	0.258
rs889550	53002	31129952	A/G			
rs750952	53064	31130014	C/T	0.43	0.41	0.535
rs2077633	53637	31130587	A/G			
rs7199949	55274	31132224	C/G	0.46	0.53	0.051
rs2032916	55825	31132775	C/T			
rs4468641	55986	31132936	A/C	0.26	0.25	0.902
rs4889535	56684	31133634	C/G			
rs4316775	57653	31134603	C/T			
rs4313819	57659	31134609	C/G			
rs6565218	57692	31134642	G/T			
rs4318224	57775	31134725	C/T			
rs1046030	61313	31138263	C/T			
rs7294	61431	31138381	A/G	0.38	0.37	0.669
rs7200749	61699	31138649	A/G			
rs2359612	62906	31139856	A/G	0.56	0.48	0.017
rs8050894	63619	31140569	C/G	0.48	0.45	0.320
rs2884737	64664	31141614	A/C	0.68	0.60	0.016
rs1895514	68452	31145402	G/T			
rs8060209	69665	31146615	C/T			
rs8060217	69681	31146631	C/T			
rs7196161	70091	31147041	A/G			
rs8062336	74637	31151587	A/G			
rs8043778	74760	31151710	A/G			
rs2032915	76523	31153473	A/G	0.43	0.41	0.505
rs4889616	78559	31155509	C/G			
rs1045564	79549	31156499	A/C			
rs2303221	79882	31156832	C/T			
rs1549296	81339	31158289	A/G			
rs889555	81681	31158631	C/T	0.49	0.50	0.740
rs5816521	81696	31158646	-/G			
rs749767	83517	31160467	C/T	0.28	0.36	0.020
rs2884738	85431	31162381	A/C			
rs2052581	86332	31163282	C/T			
rs4889617	87358	31164308	A/G			
rs4889619	87725	31164675	C/T			

dbSNP rs#	Position in SEQ ID NO: 1	Chromosome Position	A1/A2 Allele	F A2 Case AF	F A2 Control AF	F p- Value
rs1978487	89052	31166002	A/G	0.62	0.57	0.124
rs1978486	90020	31166970	A/G			
rs1978485	90231	31167181	A/G	0.90	0.88	0.513
rs4889620	90284	31167234	A/G			
rs4889621	90447	31167397	C/T			
rs3214477	90601	31167551	-/G			
rs4527034	90724	31167674	A/G	0.37	0.43	0.079
rs1060506	92559	31169509	C/T	0.29	0.28	0.720
rs7200125	95176	31172126	A/G			
rs6565219	95195	31172145	C/T			
rs889548	96822	31173772	A/G	0.54	0.51	0.320
rs6145813	Not mapped	Not mapped	/TTTTT TTTTT	0.33	0.32	0.909

[0230] Allelotyping results were considered particularly significant with a calculated p-value of less than or equal to 0.05 for allelotyping results. These values are indicated in bold. The allelotyping p-values were plotted in Figure 1A for the discovery cohort. The position of each SNP on the chromosome is presented on the x-axis. The y-axis gives the negative logarithm (base 10) of the p-value comparing the estimated allele in the case group to that of the control group. The minor allele frequency of the control group for each SNP designated by an X or other symbol on the graphs in Figure 1C can be determined by consulting Table 13. For example, the left-most X on the left graph is at position 31077197. By proceeding down the Table from top to bottom and across the graphs from left to right the allele frequency associated with each symbol shown can be determined.

[0231] To aid the interpretation, multiple lines have been added to the graph. The broken horizontal lines are drawn at two common significance levels, 0.05 and 0.01. The vertical broken lines are drawn every 20kb to assist in the interpretation of distances between SNPs. Two other lines are drawn to expose linear trends in the association of SNPs to the disease. The light gray line (or generally bottom-most curve) is a nonlinear smoother through the data points on the graph using a local polynomial regression method (W.S. Cleveland, E. Grosse and W.M. Shyu (1992) Local regression models. Chapter 8 of Statistical Models in S eds J.M. Chambers and T.J. Hastie, Wadsworth & Brooks/Cole.). The black line provides a local test for excess statistical significance to identify regions of association. This was created by use of a 10kb sliding window with 1kb step sizes. Within each window, a chi-square goodness of fit test was applied to compare the proportion of SNPs that were significant at a test wise level of 0.01, to the proportion that would be expected by chance alone (0.05 for the methods used here). Resulting p-values that were less than 10^{-8} were truncated at that value.

[0232] Finally, the exons and introns of the genes in the covered region are plotted below each graph at the appropriate chromosomal positions. The gene boundary is indicated by the broken

horizontal line. The exon positions are shown as thick, unbroken bars. An arrow is placed at the 3' end of each gene to show the direction of transcription.

Example 5

Chromosome 4 Region Proximal SNPs

[0233] SNP rs1957723 is associated with osteoarthritis and is described in Table A. One hundred-thirty additional allelic variants proximal to rs1957723 were identified and subsequently allelotyped in osteoarthritis case and control sample sets as described in Examples 1 and 2. The polymorphic variants are set forth in Table 14. The chromosome positions provided in column four of Table 14 are based on Genome “Build 34” of NCBI’s GenBank.

TABLE 14

dbSNP rs#	Chromosome	Position in SEQ ID NO: 2	Chromosome Position	Allele Variants
rs3849023	4	211	36870611	g/t
rs1444311	4	7217	36877617	a/g
rs2044295	4	7895	36878295	a/c
rs2166093	4	13308	36883708	c/t
rs2376334	4	14279	36884679	g/t
rs1444320	4	17026	36887426	c/t
rs2044294	4	18271	36888671	a/g
rs1899864	4	20417	36890817	c/t
rs1562094	4	21843	36892243	a/g
rs1562098	4	22069	36892469	a/g
rs1562097	4	22145	36892545	a/g
rs1562096	4	22519	36892919	a/g
rs1562095	4	22539	36892939	a/g
rs1444319	4	23236	36893636	a/c
rs1444318	4	23256	36893656	a/c
rs1025938	4	23402	36893802	c/t
rs1025937	4	23499	36893899	a/c
rs1025936	4	23620	36894020	c/t
rs1020333	4	23871	36894271	a/t
rs2120654	4	24136	36894536	c/g
rs2588547	4	25427	36895827	a/g
rs2044293	4	25866	36896266	g/t
rs2760324	4	26541	36896941	a/g
rs2588546	4	26576	36896976	g/t
rs2588545	4	26689	36897089	a/g
rs2760328	4	26720	36897120	a/c
rs2588544	4	27113	36897513	c/t
rs2760331	4	27164	36897564	c/t
rs2588543	4	27186	36897586	a/g
rs2588542	4	28341	36898741	a/t

dbSNP rs#	Chromosome	Position in SEQ ID NO: 2	Chromosome Position	Allele Variants
rs2588541	4	29160	36899560	c/t
rs2588540	4	29844	36900244	a/g
rs2760336	4	30665	36901065	g/t
rs2760337	4	30830	36901230	a/g
rs2028732	4	31061	36901461	a/c
rs2588538	4	31523	36901923	c/t
rs1992617	4	32326	36902726	c/t
rs1998469	4	32346	36902746	a/g
rs1998470	4	32358	36902758	c/t
rs1975498	4	34909	36905309	c/t
rs1562093	4	34975	36905375	a/g
rs1975497	4	35066	36905466	c/t
rs1562092	4	35096	36905496	g/t
rs2248788	4	35375	36905775	c/t
rs1899862	4	36304	36906704	a/g
rs2588532	4	36712	36907112	a/t
rs1885878	4	36770	36907170	c/t
rs986648	4	37342	36907742	c/t
rs986647	4	37412	36907812	c/t
rs1010010	4	37884	36908284	a/g
rs1010009	4	38077	36908477	a/c
rs2760325	4	38300	36908700	c/t
rs2588531	4	38301	36908701	c/t
rs1838388	4	41189	36911589	c/t
rs1975495	4	44408	36914808	c/t
rs2181491	4	44493	36914893	a/c
rs1975496	4	44571	36914971	a/g
rs2181492	4	44670	36915070	a/g
rs2224719	4	45219	36915619	a/g
rs2224720	4	45258	36915658	c/t
rs1951770	4	47261	36917661	a/g
rs2296040	4	48473	36918873	a/c
rs1957723	4	48771	36919171	a/g
rs1957725	4	55292	36925692	c/t
rs2889346	4	56479	36926879	a/g
rs1885879	4	56747	36927147	a/c
rs1957726	4	60620	36931020	g/t
rs1957727	4	60688	36931088	a/c
rs1885880	4	61058	36931458	a/c
rs1885881	4	61129	36931529	c/t
rs942108	4	61577	36931977	c/t
rs1951771	4	61961	36932361	a/g
rs2376323	4	63351	36933751	g/t
rs2013358	4	63926	36934326	a/g
rs2181494	4	65798	36936198	a/g
rs1957728	4	66043	36936443	a/c
rs1957729	4	66044	36936444	a/g

dbSNP rs#	Chromosome	Position in SEQ ID NO: 2	Chromosome Position	Allele Variants
rs1957730	4	66246	36936646	c/t
rs1957731	4	66318	36936718	c/t
rs1998468	4	66547	36936947	g/t
rs1957732	4	71238	36941638	c/t
rs1957733	4	71283	36941683	a/g
rs2376322	4	71492	36941892	a/g
rs2889345	4	72274	36942674	a/g
rs1815267	4	73762	36944162	a/t
rs1957734	4	74209	36944609	g/t
rs1957735	4	75284	36945684	a/t
rs1957736	4	77347	36947747	a/c
rs1957737	4	77589	36947989	c/t
rs1957738	4	78096	36948496	a/g
rs1957739	4	78606	36949006	a/g
rs1957740	4	78862	36949262	g/t
rs1957741	4	79135	36949535	a/g
rs1957742	4	79146	36949546	a/g
rs1957743	4	79456	36949856	c/t
rs1957744	4	79609	36950009	a/g
rs1957745	4	80086	36950486	a/g
rs1957746	4	80119	36950519	a/g
rs1957747	4	80766	36951166	c/t
rs2146670	4	81110	36951510	a/g
rs2146671	4	81269	36951669	a/t
rs1957748	4	81668	36952068	c/t
rs2162307	4	82433	36952833	c/t
rs1962839	4	82559	36952959	c/g
rs2376315	4	83298	36953698	c/t
rs1426410	4	83821	36954221	a/g
rs1895921	4	84121	36954521	c/t
rs1895922	4	84147	36954547	c/t
rs1035779	4	84543	36954943	a/g
rs1035780	4	84554	36954954	a/g
rs1035781	4	84691	36955091	a/g
rs1035782	4	84727	36955127	a/g
rs1426411	4	85678	36956078	c/t
rs1834602	4	86699	36957099	c/t
rs1834603	4	86700	36957100	a/g
rs1834604	4	86792	36957192	a/g
rs1834605	4	86832	36957232	a/g
rs2162308	4	87045	36957445	a/g
rs1365341	4	87140	36957540	a/g
rs1820458	4	87365	36957765	a/c
rs1469310	4	88342	36958742	c/t
rs3057879	4	88498	36958898	-/tca
rs1469311	4	88589	36958989	a/g
rs768326	4	95502	36965902	a/g

dbSNP rs#	Chromosome	Position in SEQ ID NO: 2	Chromosome Position	Allele Variants
rs1863523	4	96968	36967368	c/t
rs1469312	4	97448	36967848	c/t
rs1469313	4	97568	36967968	c/t
rs1951773	4	98724	36969124	c/t
rs2120655	4	Not mapped	Not mapped	t/g
rs2181495	4	Not mapped	Not mapped	g/a

Assay for Verifying and Allelotyping SNPs

[0234] The methods used to verify and allelotype the 130 proximal SNPs of Table 14 are the same methods described in Examples 1 and 2 herein. The primers and probes used in these assays are provided in Table 15 and Table 16, respectively.

TABLE 15

dbSNP rs#	Forward PCR primer	Reverse PCR primer
rs3849023	ACGTTGGATGGGTAATTGCTAACCATGTTT	ACGTTGGATGGACCCAGTCAAGTCAATAAAC
rs1444311	ACGTTGGATGGCCTATTGGTTTAACTAGGC	ACGTTGGATGTCTGGCTTCTTCAGGAGTTC
rs2044295	ACGTTGGATGCCACACCACTACTATTCAAG	ACGTTGGATGGTGGTGTGTTAGAAGGTTAC
rs2166093	ACGTTGGATGAAAATCCTGGAGATGGATGG	ACGTTGGATGTAGGTGTACAGTTCAGTGTCT
rs2376334	ACGTTGGATGTCTCAGAGAACCAGCTTTTG	ACGTTGGATGGGGAATATTAACATTGGGG
rs1444320	ACGTTGGATGTAATTCTCTCCTCCAAATGC	ACGTTGGATGCTAGAAACAAAAGACTACATG
rs2044294	ACGTTGGATGAACCTAAATCTCCTCAAGCC	ACGTTGGATGTTCTGACCACTTCTCTATGG
rs1899864	ACGTTGGATGTTTATAGGCGTGGGCAATCG	ACGTTGGATGTTGTGAGAAAGTGTCTGTC
rs1562094	ACGTTGGATGTGGATTCTTTCTTGAAGAC	ACGTTGGATGGCAACAAAGAACTTAATGC
rs1562098	ACGTTGGATGTCTGAGTCCGAGTGATCATC	ACGTTGGATGAAACAATTAGCAGGGCACAG
rs1562097	ACGTTGGATGCACAGGATCTTACTCTGTTG	ACGTTGGATGCGGACTCAGAAATTCAAGTC
rs1562096	ACGTTGGATGACCCAGGGCATGTTATATAG	ACGTTGGATGTTTCTCTCTGGTACCCTCTC
rs1562095	ACGTTGGATGTGTTAGTAACCCAGGGCATG	ACGTTGGATGTGACAGATGCCACCAGTTAC
rs1444319	ACGTTGGATGTTCAACTTTAGCCTCTGGGC	ACGTTGGATGCCCTGCAAAGTCAAAGGAAC
rs1444318	ACGTTGGATGCTCTGGGCAATTATCAAGCC	ACGTTGGATGAGTTCGCTGATGTGTTGGG
rs1025938	ACGTTGGATGCAGGTAAGAAAAGCTTTTGG	ACGTTGGATGCCCTGCTAATGACTGAATTC
rs1025937	ACGTTGGATGGAATAGGAAAGGTAGTATACC	ACGTTGGATGAAATTCAGTCATTAGCAGGG
rs1025936	ACGTTGGATGTCTCCAGGTAGATGAGTCAG	ACGTTGGATGCCACACACCAAGCAATCAC
rs1020333	ACGTTGGATGGCATCTCTTCAATCTGGACG	ACGTTGGATGGTGGATCACAGAAGTCAGAG
rs2120654	ACGTTGGATGACCAGAAAGACCAGGGCATG	ACGTTGGATGAACCTTTAGCTCTTCTCCCC
rs2588547	ACGTTGGATGTCACAAATGTAATATAAATC	ACGTTGGATGGATAGCTACGTTTAAAAATG
rs2044293	ACGTTGGATGTGTCAACAATACAAGACTAA	ACGTTGGATGTGCACTGGACTTTTTTTTTT
rs2760324	ACGTTGGATGACAAACCAAGTGGTTGAGGAG	ACGTTGGATGCCTCACGAATCCAACAGAAC
rs2588546	ACGTTGGATGCTTAGAGGATGGAGTCAGTC	ACGTTGGATGTACTACCAGAGATGCTGGTG
rs2588545	ACGTTGGATGCAACACAGCTACAGTGCATC	ACGTTGGATGTGGGTAAAGGGAAAAGAAGG
rs2760328	ACGTTGGATGGCCATAAAATTGGGTAAAGGG	ACGTTGGATGGCATCTATTTGACACCAACG
rs2588544	ACGTTGGATGTAAGAATTAGCATGTGAAAG	ACGTTGGATGTTTGTGCACAAAGAATTTGG
rs2760331	ACGTTGGATGAAACAGTATGCCTTTTGTGC	ACGTTGGATGCTTCTCGTAATTTTACATGAC

dbSNP rs#	Forward PCR primer	Reverse PCR primer
rs2588543	ACGTTGGATGGTGCCAAATTCTTTGTGCAC	ACGTTGGATGCTAAGATAGGTAGATACCAG
rs2588542	ACGTTGGATGTGGCAGCAAAGCTTAAGCTC	ACGTTGGATGTCCACAGTCACCTCTCATT
rs2588541	ACGTTGGATGTGACAAGGTCTATGTCAGGG	ACGTTGGATGGGCATTGTGTCATGGTGATGAG
rs2588540	ACGTTGGATGTGCTGTATGATCCAGCAATC	ACGTTGGATGGGTGCAAATACTGTCTCTTC
rs2760336	ACGTTGGATGAAGCTGAGGCAGGAGAATGG	ACGTTGGATGTGTTTTGAGACGGAGTCTCG
rs2760337	ACGTTGGATGGGTGTTTGAAGTATACAAG	ACGTTGGATGACTACCATTCTACTCTCTGC
rs2028732	ACGTTGGATGTTCTTGGACAGCTAAATAGG	ACGTTGGATGGCCATTGTGCTTTTCTTGTT
rs2588538	ACGTTGGATGTATCTTCTGGGAAGCCTTTC	ACGTTGGATGGACTTGAAATCACTCCATGC
rs1992617	ACGTTGGATGGGAGGACATTGCCTTCAAAG	ACGTTGGATGCTGACCTTCTGTCTAGTCAC
rs1998469	ACGTTGGATGTATATGCCAAGGACCAACGG	ACGTTGGATGCTGACCTTCTGTCTAGTCAC
rs1998470	ACGTTGGATGATTTCCCCCATTAAAGCTTTG	ACGTTGGATGGAAAAGTATTATATGCCAAGG
rs1975498	ACGTTGGATGAGCTCTCTTTTGCCTGCTG	ACGTTGGATGAGGAGGCTTCACAATCATGG
rs1562093	ACGTTGGATGTGATTGTGAAGCCTCCTCTG	ACGTTGGATGAAAGACATACCCAAGACTGG
rs1975497	ACGTTGGATGTCAGCAGCATGAAAAGTAC	ACGTTGGATGCATTAGACTTTTTCTGGGG
rs1562092	ACGTTGGATGTTCCAGTGACTGGACCATAG	ACGTTGGATGTCAGCAGCATGAAAAGTAC
rs2248788	ACGTTGGATGGGGAAAAGAAAAAGACTTCC	ACGTTGGATGGTAGTAGCTGCTTCTAAAAG
rs1899862	ACGTTGGATGTAATCTCCCATATAAAGTGC	ACGTTGGATGGCTACAAAAGAAAATGAATAC
rs2588532	ACGTTGGATGCAAACAATAGTGGCTGAGAG	ACGTTGGATGTTTGTAGCACAGGCGCATAG
rs1885878	ACGTTGGATGTGACTCAGCGAGTTTGTAGC	ACGTTGGATGAGCCAGATTGGGTGCTTTTC
rs986648	ACGTTGGATGTGAGAAAGCTTTCTGAGGAC	ACGTTGGATGGGTTTTCTGTTGTGAATGGG
rs986647	ACGTTGGATGACACACTCTTCTCAAGCAG	ACGTTGGATGCTTATTGTCTCAGAAAGC
rs1010010	ACGTTGGATGACTGTAGCTAAGTTGGCAT	ACGTTGGATGTTACCAACACCAATAAGGC
rs1010009	ACGTTGGATGTCTCATCAGCTCTTTCCTGG	ACGTTGGATGAAAGGGATGAGGAAGTGAGG
rs2760325	ACGTTGGATGATCCCCAGCATGTAGCATAG	ACGTTGGATGCTGCCCATAGTCTCTTCTG
rs2588531	ACGTTGGATGATCCCCAGCATGTAGCATAG	ACGTTGGATGCTGCCCATAGTCTCTTCTG
rs1838388	ACGTTGGATGGTACCTCATGGATATTACAC	ACGTTGGATGTTGGTGTGTTATAAATGAC
rs1975495	ACGTTGGATGCAGGTCAGGAGTTTAAGACC	ACGTTGGATGAGCTGGGATTACAGTCATGC
rs2181491	ACGTTGGATGGTACCTAATATATGCTTCTGG	ACGTTGGATGTTATTCCCGTCTTACTTTCC
rs1975496	ACGTTGGATGTATATTAGGTACAGTGTGGC	ACGTTGGATGCAACCAACTTCACTGAAAGC
rs2181492	ACGTTGGATGCTTGCAAGGAAGAGGAAGAAG	ACGTTGGATGACAATCACCTTTGGAGGCAG
rs2224719	ACGTTGGATGTCAAGGGTGTAGATGTGTAG	ACGTTGGATGCCAGAGAGGAGTAATGGTAT
rs2224720	ACGTTGGATGCCAATTACTCAAGGGTGTAG	ACGTTGGATGAATTCAGTACAGACAGAGGG
rs1951770	ACGTTGGATGCCTGGGAACCTTCAGCTTTTC	ACGTTGGATGTGGCACAGCAGGAATATCAG
rs2296040	ACGTTGGATGGGGCATCATGAAATGCAGAC	ACGTTGGATGGCATGTACAGGAAAGCAGTG
rs1957723	ACGTTGGATGTACTCACTTGTGTACTGCTC	ACGTTGGATGGCTGCAGCGTCACATTAATC
rs1957725	ACGTTGGATGTTATTGGAATTCCTCAGGTC	ACGTTGGATGAAGATGATTAGTCCAGCCTG
rs2889346	ACGTTGGATGTGACTGACTTCCTAGGTCAG	ACGTTGGATGTGACAGTGTGAGTGGCAG
rs1885879	ACGTTGGATGTTACCCCTTCACATCTGAT	ACGTTGGATGCTACAAGGAAGATAACAGAG
rs1957726	ACGTTGGATGAAATTCAGCCACTCAACCAG	ACGTTGGATGAAGTGGTTGGGATTTGTGAG
rs1957727	ACGTTGGATGGCCAACGTATCTTTAAACCC	ACGTTGGATGGTTTTGTCTTGGTTCTCATC
rs1885880	ACGTTGGATGTGGAATGCCCAAGATTTCA	ACGTTGGATGCTGGAATCCCAAGGTTCTCTG
rs1885881	ACGTTGGATGTAGACGTGTTCTGCATCATG	ACGTTGGATGATGAAATCTTGGGGCATTCC
rs942108	ACGTTGGATGGAGCTGTTAGGGTAGAAATG	ACGTTGGATGGTCTTGGACTAATTTTGACC
rs1951771	ACGTTGGATGGGCATTCCCTTTTGTCTAAG	ACGTTGGATGAGTAAACAAGGACTAGAGCC
rs2376323	ACGTTGGATGTCCTTACTTGCTAGCACTGC	ACGTTGGATGGCATCCCTTGGTGACTGATA
rs2013358	ACGTTGGATGGGAATTTTAGGAGTACTGTAG	ACGTTGGATGGCCAACCATAGAACCTAAATC
rs2181494	ACGTTGGATGATTCAATTACCTCCCACTGG	ACGTTGGATGTATCCCCACCAATGTACAC

dbSNP rs#	Forward PCR primer	Reverse PCR primer
rs1957728	ACGTTGGATGAAATAGATCCCAACCAAGGG	ACGTTGGATGGTAACATTACCTAAGCGGG
rs1957729	ACGTTGGATGAAATAGATCCCAACCAAGGG	ACGTTGGATGGTAACATTACCTAAGCGGG
rs1957730	ACGTTGGATGGGTCTAAACATGAGAGACTC	ACGTTGGATGTCTTTATGGATATAGGGTCC
rs1957731	ACGTTGGATGTATTGGAACCTGGTACCTGG	ACGTTGGATGGACCTGAATCATGTCTCCAG
rs1998468	ACGTTGGATGTATAAAGCCTCAAAAGTGGG	ACGTTGGATGACCTTATTCCAGAATGAAAC
rs1957732	ACGTTGGATGAAGAGAGGAGTTTATTGGCC	ACGTTGGATGCGGCCTGATCTTTATTTTCG
rs1957733	ACGTTGGATGCTATCAAGACTCTGATTGCC	ACGTTGGATGTGTTTGCAGGTAAACTTGGC
rs2376322	ACGTTGGATGTCGTTCTCTCTCTGTGCATG	ACGTTGGATGTTAGTCAGATGCTTGGTGAG
rs2889345	ACGTTGGATGTGGAATCCCAAACCTTTTTCAG	ACGTTGGATGTTCTTGCTAAATGTAGGCC
rs1815267	ACGTTGGATGCAGGAAAGGGCTACTATCAG	ACGTTGGATGGTAGGCCAAACTAGCTTTGG
rs1957734	ACGTTGGATGCTACCCCTGCCTTATAATTC	ACGTTGGATGCAAGTGGTAAAAGGATGTGG
rs1957735	ACGTTGGATGAGCTTCCCATGGTTATAGAG	ACGTTGGATGCTGAAAACAATACCGGTCTC
rs1957736	ACGTTGGATGCTGAAGCAAAGATTTCTCTC	ACGTTGGATGAGCATCTTTTGCTGTCACTG
rs1957737	ACGTTGGATGACATGGAAGCTGAAGCCAAG	ACGTTGGATGCAGAGCTTTGACCTTACTCC
rs1957738	ACGTTGGATGATGTCCCTTAAAAGGCTGCC	ACGTTGGATGCAGATGATCTTGCTTCCAG
rs1957739	ACGTTGGATGTCACTGCCTGAGTGCTTTAG	ACGTTGGATGCTGATGGCCTGAGAACTAAG
rs1957740	ACGTTGGATGGCCCAGTCAAGTTGACATAC	ACGTTGGATGCACCTGCTCCAGTTATATAC
rs1957741	ACGTTGGATGAGGAGCATTATCCCTATTAG	ACGTTGGATGCCTCTTAGTAAAATATGGATG
rs1957742	ACGTTGGATGGGATGATATCTACTTTGTACG	ACGTTGGATGGACTCCATCTGAGATGTTAG
rs1957743	ACGTTGGATGCAACTGTCTTGATTTGAAG	ACGTTGGATGGACAGACTTTTCATTGTTTTTC
rs1957744	ACGTTGGATGTCAGTGTACCCTGTAATGCC	ACGTTGGATGTGCCAGCAGTGAGTAATTG
rs1957745	ACGTTGGATGGTTTAGAAAGTGTGGGTTCC	ACGTTGGATGAGCAAATGCAGCTTATTACC
rs1957746	ACGTTGGATGTCTCATACAACATAGTTAGC	ACGTTGGATGGGTTTAGGTTTGGTTTGATG
rs1957747	ACGTTGGATGGTCACTCAAGATAACAGTTCC	ACGTTGGATGTTACCTAACGTGAAGGTAGC
rs2146670	ACGTTGGATGCCTAACACATCTTTATGAGC	ACGTTGGATGCTCATAAGATATGCTAAGCAC
rs2146671	ACGTTGGATGATGAGGAGCAACTAGAAGGC	ACGTTGGATGAAAGGGCTGGAAGAAACAGG
rs1957748	ACGTTGGATGTGAAGTTTGTAGTAGGGAGC	ACGTTGGATGTTCTGTACACAAACACTCC
rs2162307	ACGTTGGATGACATGCGGTGCCTGGCCCTTT	ACGTTGGATGCCTTTGTAGGGACATGGATG
rs1962839	ACGTTGGATGGGCTGCATAGTATTCCATGG	ACGTTGGATGAGGGAATCCTTTCCCCATTG
rs2376315	ACGTTGGATGTGGCCTTGGATTTCTTCCAC	ACGTTGGATGAGAATTGGACAGAGTGGCAG
rs1426410	ACGTTGGATGGAGAAAGTTGCATCTTGCCC	ACGTTGGATGGGGAAGTTTTACCTTGGCTC
rs1895921	ACGTTGGATGGGTGATGGTGTTTGAGGTAC	ACGTTGGATGATTAGGCTTCTCCCACCATC
rs1895922	ACGTTGGATGCAATGCATTAGGCTTCTCCC	ACGTTGGATGGAGGTACATTTCTCAGGCAG
rs1035779	ACGTTGGATGGAGAATCACTTGAACCCGGG	ACGTTGGATGTGGAGTGCAGTGGCATGATC
rs1035780	ACGTTGGATGTTTGAGATGGAGTCTCGCTC	ACGTTGGATGAATCACTTGAACCCGGGAGG
rs1035781	ACGTTGGATGGGAAGATGCTGACTCTGAAC	ACGTTGGATGCCTTGACTGTTTAGGGATCC
rs1035782	ACGTTGGATGGGATCCCTAAACAGTCAAGG	ACGTTGGATGAGTTGGCTAGACTTGCGTTC
rs1426411	ACGTTGGATGCAAGAGTGCTACACAAGTCG	ACGTTGGATGTGTACCTTGCTCAGGTGATC
rs1834602	ACGTTGGATGGATGGGCCCTATTTTCTTG	ACGTTGGATGCTTTTCCAACCCAGTAATGTC
rs1834603	ACGTTGGATGGATGGGCCCTATTTTCTTG	ACGTTGGATGTCTTTTCCAACCCAGTAATG
rs1834604	ACGTTGGATGGAAAGACATTACTGGGTTGG	ACGTTGGATGAGAATTCTTCTGACTGTGG
rs1834605	ACGTTGGATGGCCACAGTCAGGAAGAATT	ACGTTGGATGTTGTGGAGACTGGCCAAAAG
rs2162308	ACGTTGGATGTAAAGAAACAGAGGGACACC	ACGTTGGATGTATGATCAGAGTCATCAGGG
rs1365341	ACGTTGGATGTCCCTCTGTTTCTTTAGGCA	ACGTTGGATGCATCTCCCCTGGTAGCATTT
rs1820458	ACGTTGGATGCACCCTCAGACTTGGAAATG	ACGTTGGATGGTCAGGTGACTCTATTTCAGC
rs1469310	ACGTTGGATGTACTACAGCGTGTTTAGCAG	ACGTTGGATGTGTCAAAGGGAGAGTTAGAG
rs3057879	ACGTTGGATGGGCACATTGGAATAAAGCC	ACGTTGGATGACGGCATGAACAATTCTCAG

dbSNP rs#	Forward PCR primer	Reverse PCR primer
rs1469311	ACGTTGGATGCCTGAGAATTGTTTCATGCCG	ACGTTGGATGTTTTCACTGTTCTCTCCAGG
rs768326	ACGTTGGATGAATTAGCCAGGCATGGTGTG	ACGTTGGATGACATCCTAGGCTCAAGTGAC
rs1863523	ACGTTGGATGGGCAGACACATTCTTATTCG	ACGTTGGATGGGGAAAAGGTGTGCTGAGTAA
rs1469312	ACGTTGGATGCATTTTCGTCAGCATTCTAGC	ACGTTGGATGGGACTCATGTCTCTCTTTGG
rs1469313	ACGTTGGATGAGTGAGGGAGAAAAGTGAAC	ACGTTGGATGCCTAACTTCTCTCCAATCTC
rs1951773	ACGTTGGATGAAGGTTCAAGTTACCGCATG	ACGTTGGATGCACTGTGGTCCATGAAAAA
rs2120655	ACGTTGGATGACAGGGTTTCTGCATGTTGC	ACGTTGGATGACGCCTGTAATCCAGCACT
rs2181495	ACGTTGGATGGAATTGTGGGAGTTACAATTC	ACGTTGGATGGAATCAAGCTAATTAACATGTG

TABLE 16

dbSNP rs#	Extend Primer	Term Mix
rs3849023	CTCATAACATAAGAAGTTGATGC	CGT
rs1444311	CTAGGCATGCTAGCTTGGC	ACT
rs2044295	CACTACTATTCAAGATTACCTTT	ACT
rs2166093	GGTGGTGATGGCTGCACAA	ACG
rs2376334	TCAGAGAACCAGCTTTTGATTTCA	ACT
rs1444320	GCCTAGACCCCGTGCAAC	ACG
rs2044294	CTCCTCAAGCCAATAGGTCTTA	ACG
rs1899864	CGCACCTGGCCGAAAATAAC	ACT
rs1562094	AACCTGCAAAAGATTTACACTTGC	ACT
rs1562098	TCCTGCCTCAGCCTTCCTAGA	ACT
rs1562097	ACTCTGTTGTTTCAGGCTGGGGT	ACT
rs1562096	TAAGCTAGCTAGTAAGTGGTG	ACT
rs1562095	ATGTTATATAGAACATCCCTTTTT	ACT
rs1444319	TCTGGGCAATTATCAAGCCTTT	ACT
rs1444318	CTTTGCATTTTCCTGAGTTCCTTT	ACT
rs1025938	AAGAAAAGCTTTTTGTTTGGG	ACT
rs1025937	GGTAGTATACCTAAAAAACAGC	CGT
rs1025936	TCAAAGGACACCCAGCATTCA	ACG
rs1020333	ACGTTTATCTGTAACCTTTCCA	CGT
rs2120654	GAAAGACCAGGGCATGATTAGA	ACT
rs2588547	ACAAATGTAATATAAATCAAGCTC	ACG
rs2044293	ACCAGCCTGGGTAACATAGCCA	ACT
rs2760324	GGTTGAGGAGAAGCACCAGCA	ACG
rs2588546	TACAATTTCTAGCCTTAATAAGAT	ACT
rs2588545	TACAGTGCATCTATTTGACACCAA	ACG
rs2760328	AAATTGGGTAAAGGGAAAAGAAG	ACT
rs2588544	ATTAGCATGTGAAAGACTTCTC	ACT
rs2760331	AGTATGCCTTTTGTGCACAAAGA	ACT
rs2588543	ATTCTTTGTGCACAAAAGGCATA	ACG
rs2588542	GCTTAAGCTCTTACAGGCAG	CGT
rs2588541	AGGTCTATGTCAGGGAAAACCTTA	ACG

dbSNP rs#	Extend Primer	Term Mix
rs2588540	GATCCAGCAATCCCACTGAT	ACG
rs2760336	AGGCGGAGCTTGCAGTGAG	ACT
rs2760337	CACCAATACTGTATGATTCTTTT	ACT
rs2028732	CAGCTAAATAGGGCTTGAGTCAAT	CGT
rs2588538	AATTTGTACAAATTTATGGGGTAT	ACT
rs1992617	ATTGCCTTCAAAGAACATCAAAGC	ACG
rs1998469	GACCAACGGGAGGACATTG	ACG
rs1998470	CTTTGAAGGCAATGTCCTCC	ACG
rs1975498	TTTTGCCTGCTGCTATCCAC	ACT
rs1562093	CTCCTCTGCCATGTGGAAC	ACG
rs1975497	AAACTGACTAATACACACTGTT	ACT
rs1562092	TTTGGTTAATGGACATTTAGACT	ACT
rs2248788	TGTGGGATTTTATTATTTTCATCA	ACT
rs1899862	TAAGTGCATAACTTGTCTTTGAGG	ACT
rs2588532	ATAGTGGCTGAGAGCCAGAT	CGT
rs1885878	GCGAGTTTGTAGCACAGGC	ACT
rs986648	GTACATGTAATGCTAGTAAAGAAA	ACG
rs986647	CTCTTTCTCAAGCAGGAGTTA	ACG
rs1010010	AGCTAAGTTGGCATGTGGGA	ACT
rs1010009	CCTGGCTACCTTCCAAAAAG	ACT
rs2760325	TCTCAGGAAGTATGAAATAAATAG	ACG
rs2588531	CTCAGGAAGTATGAAATAAATAGT	ACT
rs1838388	TCATGGATATTTACACCTACTAC	ACT
rs1975495	AGGAGTTTAAGACCAGCCTG	ACT
rs2181491	TGCTTCTGGATTTTAAATGATCAC	ACT
rs1975496	ATGATCAAATCATTTTGAGGGC	ACT
rs2181492	GTTGCATTGCTATGGTCTGC	ACT
rs2224719	CATATATCCCTCTGTCTGTAC	ACG
rs2224720	GGGTGTAGATGTGTAGATTTATA	ACT
rs1951770	ACAAGCATTAGAGACTTGATTG	ACG
rs2296040	CTTTGTTTCTAAAATCTGATAGTC	ACT
rs1957723	AGCATGGCATAGGCACTGG	ACG
rs1957725	GCGAGGAAAGACCTGTTCTA	ACG
rs2889346	GGTCAGCTCAGCTGGTTTTT	ACG
rs1885879	CACATCTGATGCTCTCCTAAA	ACT
rs1957726	GCCACTCAACCAGTAGGAAA	ACT
rs1957727	GTATCTTTAAAACCCTCACAAAT	CGT
rs1885880	TTACGTTAGTCTGCCTACTTCCA	ACT
rs1885881	TGGGCTATCAATGATGGAAAC	ACT
rs942108	AAATGAAATAGAATTGTGTACTTC	ACT
rs1951771	TCCCTTTTGTCTAAGAATATTAG	ACG
rs2376323	CTAGCACTGCCAAGTGCAAC	ACT
rs2013358	TTTTAGGAGTACTGTAGAACACA	ACG
rs2181494	TGGGTCCCTCCCATAACAC	ACT

dbSNP rs#	Extend Primer	Term Mix
rs1957728	AGAAGCATGTGCTTATAACAATAA	CGT
rs1957729	GAAGCATGTGCTTATAACAATAAA	ACT
rs1957730	ACATGAGAGACTCTGAAGACT	ACT
rs1957731	GGGTGAGCTTTGGGATCAC	ACT
rs1998468	GGGCATAATTAATCCATGTTAG	ACT
rs1957732	GGCCAAGTTTACCTGCAAAC	ACT
rs1957733	TCTAATGTTAAAGAGAGGAGTTTA	ACG
rs2376322	GCGCCAAGGAAAGGCCAC	ACT
rs2889345	TCATTCTCACCCTTGATATCCA	ACT
rs1815267	AAAGGGCTACTATCAGTTTTGT	CGT
rs1957734	CTGCCTTATAATTCTAAAAAGGT	ACT
rs1957735	CTAAACTAAGAAATGTTTCCAC	CGT
rs1957736	TAATACTAAGGAGAGGGCTCCT	ACT
rs1957737	AGCCAAGGGTGTGGATGAG	ACT
rs1957738	CCTTAAAGGCTGCCTACAAAATA	ACT
rs1957739	CTGAGTGCTTTAGCTGGATTA	ACG
rs1957740	TTAAGCATCACACTGAGTTTGAG	ACT
rs1957741	AGCTGAATTAAGCGCGACAGCTA	ACG
rs1957742	TCTACTTTGTACGTAGCTGTCGC	ACT
rs1957743	GAAAATATTACTAAAAAGACCTC	ACG
rs1957744	TGTACCCTGTAATGCCTAAAGC	ACG
rs1957745	TTTTCAAAGGTTTAGGTTTGTTT	ACT
rs1957746	ACAACATAGTTAGCAAATGCAG	ACG
rs1957747	GATAACAGTTCCAATTACAACAA	ACG
rs2146670	ATCTTTATGAGCTTTTCCTTTCTT	ACG
rs2146671	TACAACCCTTTCAGGACTTCA	CGT
rs1957748	TTGTAGTAGGGAGCCATGGT	ACT
rs2162307	CCTGGCCCTTTGTCCCTG	ACG
rs1962839	CCACATCTTTGACAAACCTGA	ACT
rs2376315	CCCCCTTCTTTTCCAGGC	ACT
rs1426410	CATCTTGCCCTAAAATCACTC	ACG
rs1895921	GTACATTTCTCAGGCAGCTC	ACG
rs1895922	ATTAGGCTTCTCCCACCATC	ACT
rs1035779	ACCCGGGAGGGTTGCAGT	ACT
rs1035780	GGCTGGAGTGCAGTGCCA	ACG
rs1035781	ACCTAGACTAAGAGAGTGATTGCA	ACT
rs1035782	CCTAAACAGTCAAGGCAAAGG	ACT
rs1426411	TTTATGGTCTTCTTAGGATATCA	ACG
rs1834602	AGGAAGGTGCCCAGATCCT	ACG
rs1834603	AGGAAGGTGCCCAGATCCTT	ACT
rs1834604	AGTTTTCTAGTAACTTCTCTAAAA	ACT
rs1834605	ACAGTCAGGAAGAATTCTGTCT	ACT
rs2162308	CACCTACAGAGTTTAAAGTAAATTT	ACG
rs1365341	AAATCTCCTGGAGGGCTTCATAA	ACT

dbSNP rs#	Extend Primer	Term Mix
rs1820458	TGGAAATGGCAACTGAATCCT	ACT
rs1469310	ACCCACACAATGCCAATAGCAC	ACT
rs3057879	TGGAAAATAAAGCCTTTTGAGGTT	ACT
rs1469311	TGCCGTAAAGAGGAAAAGCT	ACT
rs768326	CAGCTACTCTGTAAAGCTGAA	ACT
rs1863523	ATATTCTTGCTCATCTTTCTCTAT	ACT
rs1469312	TAGTCCAGCAAACGCCAGC	ACT
rs1469313	GTGAACAAATAATGCAAGTTCAG	ACT
rs1951773	CCCTTTGGGAGAGAAGGGC	ACT
rs2120655	AGCAATCCTCCCACCTTTGGC	CGT
rs2181495	GGTGACATTTGGGTGGGATACA	ACT

Genetic Analysis

[0235] Allelotyping results from the discovery cohort are shown for cases and controls in Table 17. The allele frequency for the A2 allele is noted in the fifth and sixth columns for osteoarthritis case pools and control pools, respectively, where “AF” is allele frequency. The allele frequency for the A1 allele can be easily calculated by subtracting the A2 allele frequency from 1 (A1 AF = 1-A2 AF). For example, the SNP rs1444311 has the following case and control allele frequencies: case A1 (A) = 0.74; case A2 (G) = 0.26; control A1 (A) = 0.75; and control A2 (G) = 0.25, where the nucleotide is provided in paranthesis. Some SNPs are labeled “untyped” because of failed assays.

TABLE 17

dbSNP rs#	Position in SEQ ID NO: 2	Chromosome Position	A1/A2 Allele	F A2 Case AF	F A2 Control AF	F p- Value
rs3849023	211	36870611	G/T			
rs1444311	7217	36877617	A/G	0.26	0.25	0.566
rs2044295	7895	36878295	A/C			
rs2166093	13308	36883708	C/T			
rs2376334	14279	36884679	G/T	0.15	0.16	0.734
rs1444320	17026	36887426	C/T			
rs2044294	18271	36888671	A/G	0.16	0.14	0.412
rs1899864	20417	36890817	C/T			
rs1562094	21843	36892243	A/G	0.22	0.23	0.586
rs1562098	22069	36892469	A/G			
rs1562097	22145	36892545	A/G	NA	0.97	NA
rs1562096	22519	36892919	A/G	0.20	0.21	0.773
rs1562095	22539	36892939	A/G	0.53	0.51	0.407
rs1444319	23236	36893636	A/C	0.74	0.79	0.023
rs1444318	23256	36893656	A/C	0.12	0.13	0.559
rs1025938	23402	36893802	C/T	0.18	0.19	0.633
rs1025937	23499	36893899	A/C			
rs1025936	23620	36894020	C/T	0.84	0.84	0.907
rs1020333	23871	36894271	A/T			
rs2120654	24136	36894536	C/G	0.15	0.16	0.718
rs2588547	25427	36895827	A/G	0.39	0.40	0.603
rs2044293	25866	36896266	G/T			

dbSNP rs#	Position in SEQ ID NO: 2	Chromosome Position	A1/A2 Allele	F A2 Case AF	F A2 Control AF	F p- Value
rs2760324	26541	36896941	A/G	0.59	0.61	0.395
rs2588546	26576	36896976	G/T	0.07	0.05	0.352
rs2588545	26689	36897089	A/G			
rs2760328	26720	36897120	A/C	0.25	0.26	0.791
rs2588544	27113	36897513	C/T			
rs2760331	27164	36897564	C/T	0.91	0.94	0.184
rs2588543	27186	36897586	A/G	0.59	0.59	0.828
rs2588542	28341	36898741	A/T			
rs2588541	29160	36899560	C/T	0.61	0.59	0.313
rs2588540	29844	36900244	A/G	0.62	0.62	0.999
rs2760336	30665	36901065	G/T			
rs2760337	30830	36901230	A/G	0.16	0.16	0.826
rs2028732	31061	36901461	A/C	0.60	0.58	0.432
rs2588538	31523	36901923	C/T	0.62	0.61	0.853
rs1992617	32326	36902726	C/T	0.61	0.59	0.282
rs1998469	32346	36902746	A/G			
rs1998470	32358	36902758	C/T	0.81	0.86	0.018
rs1975498	34909	36905309	C/T			
rs1562093	34975	36905375	A/G	0.89	0.87	0.529
rs1975497	35066	36905466	C/T	0.13	0.13	0.691
rs1562092	35096	36905496	G/T			
rs2248788	35375	36905775	C/T	0.29	0.31	0.368
rs1899862	36304	36906704	A/G	0.18	0.16	0.274
rs2588532	36712	36907112	A/T	0.30	0.32	0.443
rs1885878	36770	36907170	C/T	0.35	0.35	0.866
rs986648	37342	36907742	C/T	0.74	0.73	0.679
rs986647	37412	36907812	C/T	0.78	0.76	0.263
rs1010010	37884	36908284	A/G	0.25	0.26	0.649
rs1010009	38077	36908477	A/C	0.26	0.25	0.781
rs2760325	38300	36908700	C/T			
rs2588531	38301	36908701	C/T			
rs1838388	41189	36911589	C/T	0.75	0.74	0.650
rs1975495	44408	36914808	C/T			
rs2181491	44493	36914893	A/C	0.14	0.12	0.235
rs1975496	44571	36914971	A/G	0.26	0.26	0.944
rs2181492	44670	36915070	A/G	0.11	0.09	0.311
rs2224719	45219	36915619	A/G	0.78	0.78	0.866
rs2224720	45258	36915658	C/T	0.20	0.21	0.641
rs1951770	47261	36917661	A/G	0.22	0.18	0.029
rs2296040	48473	36918873	A/C	0.41	0.43	0.459
rs1957723	48771	36919171	A/G	0.42	0.38	0.113
rs1957725	55292	36925692	C/T	0.75	0.78	0.196
rs2889346	56479	36926879	A/G	0.54	0.55	0.677
rs1885879	56747	36927147	A/C	0.44	0.48	0.123
rs1957726	60620	36931020	G/T	0.14	0.14	0.741
rs1957727	60688	36931088	A/C	0.73	0.76	0.271
rs1885880	61058	36931458	A/C	0.43	0.43	0.935
rs1885881	61129	36931529	C/T	0.12	0.11	0.681
rs942108	61577	36931977	C/T	0.49	0.52	0.317
rs1951771	61961	36932361	A/G	0.93	NA	NA
rs2376323	63351	36933751	G/T			
rs2013358	63926	36934326	A/G	0.13	0.13	0.821
rs2181494	65798	36936198	A/G	0.42	0.43	0.512
rs1957728	66043	36936443	A/C			
rs1957729	66044	36936444	A/G	0.79	0.77	0.405
rs1957730	66246	36936646	C/T	0.15	0.16	0.719
rs1957731	66318	36936718	C/T	0.14	0.16	0.413

dbSNP rs#	Position in SEQ ID NO: 2	Chromosome Position	A1/A2 Allele	F A2 Case AF	F A2 Control AF	F p- Value
rs1998468	66547	36936947	G/T	0.13	0.12	0.468
rs1957732	71238	36941638	C/T	0.10	0.10	0.841
rs1957733	71283	36941683	A/G	0.63	0.61	0.632
rs2376322	71492	36941892	A/G	0.26	0.28	0.509
rs2889345	72274	36942674	A/G	0.20	0.18	0.234
rs1815267	73762	36944162	A/T	0.46	0.45	0.674
rs1957734	74209	36944609	G/T	0.55	0.64	0.003
rs1957735	75284	36945684	A/T	0.63	0.61	0.430
rs1957736	77347	36947747	A/C	0.05	0.05	0.903
rs1957737	77589	36947989	C/T	0.71	0.75	0.164
rs1957738	78096	36948496	A/G			
rs1957739	78606	36949006	A/G			
rs1957740	78862	36949262	G/T			
rs1957741	79135	36949535	A/G	0.76	0.80	0.077
rs1957742	79146	36949546	A/G	0.95	0.96	0.500
rs1957743	79456	36949856	C/T	0.21	0.16	0.039
rs1957744	79609	36950009	A/G	0.66	0.70	0.088
rs1957745	80086	36950486	A/G	0.88	0.90	0.354
rs1957746	80119	36950519	A/G	0.40	0.44	0.120
rs1957747	80766	36951166	C/T	0.72	0.76	0.093
rs2146670	81110	36951510	A/G	0.73	0.77	0.072
rs2146671	81269	36951669	A/T	0.17	0.15	0.250
rs1957748	81668	36952068	C/T	0.16	0.14	0.407
rs2162307	82433	36952833	C/T	0.73	0.76	0.170
rs1962839	82559	36952959	C/G			
rs2376315	83298	36953698	C/T	0.62	0.66	0.179
rs1426410	83821	36954221	A/G	0.75	0.77	0.307
rs1895921	84121	36954521	C/T	0.75	0.78	0.175
rs1895922	84147	36954547	C/T	0.15	0.12	0.095
rs1035779	84543	36954943	A/G	0.66	0.64	0.649
rs1035780	84554	36954954	A/G			
rs1035781	84691	36955091	A/G	0.73	0.77	0.100
rs1035782	84727	36955127	A/G			
rs1426411	85678	36956078	C/T	0.76	0.80	0.084
rs1834602	86699	36957099	C/T	0.20	0.16	0.072
rs1834603	86700	36957100	A/G	0.94	0.92	0.326
rs1834604	86792	36957192	A/G	0.70	0.73	0.287
rs1834605	86832	36957232	A/G	0.72	0.76	0.057
rs2162308	87045	36957445	A/G			
rs1365341	87140	36957540	A/G	0.18	0.15	0.086
rs1820458	87365	36957765	A/C	0.23	0.21	0.298
rs1469310	88342	36958742	C/T	0.20	0.18	0.265
rs3057879	88498	36958898	-/TCA	0.70	0.71	0.649
rs1469311	88589	36958989	A/G	0.70	0.74	0.065
rs768326	95502	36965902	A/G			
rs1863523	96968	36967368	C/T	0.21	0.18	0.247
rs1469312	97448	36967848	C/T	0.78	0.76	0.312
rs1469313	97568	36967968	C/T	0.81	0.80	0.617
rs1951773	98724	36969124	C/T			
rs2120655	Not mapped	Not mapped	T/G			
rs2181495	Not mapped	Not mapped	G/A	0.78	0.76	0.617

[0236] The *chrom 4* proximal SNPs were also allelotyped in the replication cohorts using the methods described herein and the primers provided in Tables 15 and 16. The replication allelotyping results for replication cohort #1 and replication cohort #2 are provided in Tables 18 and 19, respectively.

TABLE 18

dbSNP rs#	Position in SEQ ID NO: 2	Chromosome Position	A1/A2 Allele	A2 Case AF	A2 Control AF	p-Value
rs3849023	211	36870611	G/T			
rs1444311	7217	36877617	A/G	0.27	0.25	0.441
rs2044295	7895	36878295	A/C			
rs2166093	13308	36883708	C/T			
rs2376334	14279	36884679	G/T	0.14	0.14	0.970
rs1444320	17026	36887426	C/T			
rs2044294	18271	36888671	A/G	0.16	0.14	0.423
rs1899864	20417	36890817	C/T			
rs1562094	21843	36892243	A/G	0.22	0.21	0.725
rs1562098	22069	36892469	A/G			
rs1562097	22145	36892545	A/G			
rs1562096	22519	36892919	A/G	0.20	0.19	0.795
rs1562095	22539	36892939	A/G	0.55	0.53	0.453
rs1444319	23236	36893636	A/C	0.70	0.80	0.003
rs1444318	23256	36893656	A/C	0.12	0.13	0.645
rs1025938	23402	36893802	C/T	0.18	0.18	0.824
rs1025937	23499	36893899	A/C			
rs1025936	23620	36894020	C/T	0.85	0.83	0.622
rs1020333	23871	36894271	A/T			
rs2120654	24136	36894536	C/G	0.16	0.16	0.914
rs2588547	25427	36895827	A/G	0.40	0.40	0.980
rs2044293	25866	36896266	G/T			
rs2760324	26541	36896941	A/G	0.57	0.61	0.287
rs2588546	26576	36896976	G/T	0.08	0.05	0.265
rs2588545	26689	36897089	A/G			
rs2760328	26720	36897120	A/C	0.25	untyped	NA
rs2588544	27113	36897513	C/T			
rs2760331	27164	36897564	C/T	0.88	0.92	0.193
rs2588543	27186	36897586	A/G	0.57	0.58	0.869
rs2588542	28341	36898741	A/T			
rs2588541	29160	36899560	C/T	0.61	0.57	0.230
rs2588540	29844	36900244	A/G	0.64	0.64	0.926
rs2760336	30665	36901065	G/T			
rs2760337	30830	36901230	A/G	0.16	0.16	0.956
rs2028732	31061	36901461	A/C	0.60	0.57	0.330
rs2588538	31523	36901923	C/T	0.62	0.61	0.747
rs1992617	32326	36902726	C/T	0.62	0.59	0.341
rs1998469	32346	36902746	A/G			
rs1998470	32358	36902758	C/T	0.78	0.88	~0.0001
rs1975498	34909	36905309	C/T			
rs1562093	34975	36905375	A/G	0.89	0.90	0.905
rs1975497	35066	36905466	C/T	0.12	0.12	0.873
rs1562092	35096	36905496	G/T			
rs2248788	35375	36905775	C/T	0.28	0.31	0.308
rs1899862	36304	36906704	A/G	0.19	0.14	0.088
rs2588532	36712	36907112	A/T	0.30	0.33	0.347
rs1885878	36770	36907170	C/T	0.36	0.34	0.362
rs986648	37342	36907742	C/T	0.74	0.75	0.773
rs986647	37412	36907812	C/T	0.78	0.77	0.693

dbSNP rs#	Position in SEQ ID NO: 2	Chromosome Position	A1/A2 Allele	A2 Case AF	A2 Control AF	p-Value
rs1010010	37884	36908284	A/G	0.25	0.26	0.690
rs1010009	38077	36908477	A/C	0.27	0.26	0.870
rs2760325	38300	36908700	C/T			
rs2588531	38301	36908701	C/T			
rs1838388	41189	36911589	C/T	0.74	0.75	0.826
rs1975495	44408	36914808	C/T			
rs2181491	44493	36914893	A/C	0.16	0.10	0.057
rs1975496	44571	36914971	A/G	0.25	0.26	0.596
rs2181492	44670	36915070	A/G	0.11	0.08	0.167
rs2224719	45219	36915619	A/G	0.78	0.79	0.705
rs2224720	45258	36915658	C/T	0.19	0.21	0.478
rs1951770	47261	36917661	A/G	0.25	0.16	0.003
rs2296040	48473	36918873	A/C	0.39	0.43	0.241
rs1957723	48771	36919171	A/G	0.44	0.36	0.027
rs1957725	55292	36925692	C/T	0.73	0.80	0.024
rs2889346	56479	36926879	A/G	0.53	0.55	0.552
rs1885879	56747	36927147	A/C	0.43	0.50	0.057
rs1957726	60620	36931020	G/T	0.14	0.14	0.918
rs1957727	60688	36931088	A/C	0.71	0.78	0.038
rs1885880	61058	36931458	A/C	0.44	0.42	0.627
rs1885881	61129	36931529	C/T	0.12	0.12	0.833
rs942108	61577	36931977	C/T	0.42	0.49	0.096
rs1951771	61961	36932361	A/G	0.93	NA	NA
rs2376323	63351	36933751	G/T			
rs2013358	63926	36934326	A/G	0.13	0.12	0.795
rs2181494	65798	36936198	A/G	0.38	0.41	0.424
rs1957728	66043	36936443	A/C			
rs1957729	66044	36936444	A/G	0.78	0.77	0.672
rs1957730	66246	36936646	C/T	0.15	0.15	0.885
rs1957731	66318	36936718	C/T	0.15	0.16	0.719
rs1998468	66547	36936947	G/T	0.14	0.10	0.243
rs1957732	71238	36941638	C/T	0.10	0.09	0.817
rs1957733	71283	36941683	A/G	0.62	NA	0.628
rs2376322	71492	36941892	A/G	0.26	0.27	0.660
rs2889345	72274	36942674	A/G	0.22	0.16	0.020
rs1815267	73762	36944162	A/T	0.46	0.48	0.626
rs1957734	74209	36944609	G/T	0.44	0.61	~0.0001
rs1957735	75284	36945684	A/T	0.63	0.63	0.792
rs1957736	77347	36947747	A/C	0.03	0.03	0.987
rs1957737	77589	36947989	C/T	0.69	0.77	0.024
rs1957738	78096	36948496	A/G			
rs1957739	78606	36949006	A/G			
rs1957740	78862	36949262	G/T			
rs1957741	79135	36949535	A/G	0.75	0.83	0.008
rs1957742	79146	36949546	A/G	0.94	0.96	0.459
rs1957743	79456	36949856	C/T	0.24	0.14	0.009
rs1957744	79609	36950009	A/G	0.63	0.72	0.006
rs1957745	80086	36950486	A/G	0.86	0.90	0.229
rs1957746	80119	36950519	A/G	0.42	0.50	0.019
rs1957747	80766	36951166	C/T	0.71	0.79	0.009
rs2146670	81110	36951510	A/G	0.72	0.81	0.004
rs2146671	81269	36951669	A/T	0.17	0.13	0.106
rs1957748	81668	36952068	C/T	0.17	0.13	0.133
rs2162307	82433	36952833	C/T	0.72	0.78	0.020
rs1962839	82559	36952959	C/G			
rs2376315	83298	36953698	C/T	0.61	0.67	0.074
rs1426410	83821	36954221	A/G	0.73	0.79	0.058

dbSNP rs#	Position in SEQ ID NO: 2	Chromosome Position	A1/A2 Allele	A2 Case AF	A2 Control AF	p-Value
rs1895921	84121	36954521	C/T	0.72	0.80	0.013
rs1895922	84147	36954547	C/T	0.17	0.11	0.014
rs1035779	84543	36954943	A/G	0.66	0.64	0.613
rs1035780	84554	36954954	A/G			
rs1035781	84691	36955091	A/G	0.71	0.78	0.059
rs1035782	84727	36955127	A/G			
rs1426411	85678	36956078	C/T	0.75	0.82	0.008
rs1834602	86699	36957099	C/T	0.22	0.15	0.020
rs1834603	86700	36957100	A/G	0.94	0.92	0.483
rs1834604	86792	36957192	A/G	0.69	0.75	0.056
rs1834605	86832	36957232	A/G	0.71	0.79	0.007
rs2162308	87045	36957445	A/G			
rs1365341	87140	36957540	A/G	0.19	0.13	0.017
rs1820458	87365	36957765	A/C	0.24	0.19	0.141
rs1469310	88342	36958742	C/T	0.22	0.17	0.061
rs3057879	88498	36958898	-/TCA	0.67	NA	NA
rs1469311	88589	36958989	A/G	0.67	0.76	0.006
rs768326	95502	36965902	A/G			
rs1863523	96968	36967368	C/T	0.22	0.17	0.103
rs1469312	97448	36967848	C/T	0.80	0.77	0.236
rs1469313	97568	36967968	C/T	0.83	0.80	0.422
rs1951773	98724	36969124	C/T			
rs2120655	Not mapped	Not mapped	T/G			
rs2181495	Not mapped	Not mapped	G/A	0.78	0.76	0.617

TABLE 19

dbSNP rs#	Position in SEQ ID NO: 2	Chromosome Position	A1/A2 Allele	A2 Case AF	A2 Control AF	p-Value
rs3849023	211	36870611	G/T			
rs1444311	7217	36877617	A/G	0.25	0.26	0.876
rs2044295	7895	36878295	A/C			
rs2166093	13308	36883708	C/T			
rs2376334	14279	36884679	G/T	0.16	0.18	0.532
rs1444320	17026	36887426	C/T			
rs2044294	18271	36888671	A/G	NA	0.15	NA
rs1899864	20417	36890817	C/T			
rs1562094	21843	36892243	A/G	NA	0.28	NA
rs1562098	22069	36892469	A/G			
rs1562097	22145	36892545	A/G			
rs1562096	22519	36892919	A/G	0.20	0.23	0.364
rs1562095	22539	36892939	A/G	0.50	0.48	0.588
rs1444319	23236	36893636	A/C	0.79	0.79	0.923
rs1444318	23256	36893656	A/C	0.12	0.13	0.711
rs1025938	23402	36893802	C/T	0.18	0.22	0.247
rs1025937	23499	36893899	A/C			
rs1025936	23620	36894020	C/T	0.84	0.86	0.403
rs1020333	23871	36894271	A/T			
rs2120654	24136	36894536	C/G	0.14	0.16	0.682
rs2588547	25427	36895827	A/G	0.37	NA	
rs2044293	25866	36896266	G/T			
rs2760324	26541	36896941	A/G	0.60	0.60	0.965
rs2588546	26576	36896976	G/T	0.05	0.06	0.797
rs2588545	26689	36897089	A/G			
rs2760328	26720	36897120	A/C	0.25	0.26	0.816

dbSNP rs#	Position in SEQ ID NO: 2	Chromosome Position	A1/A2 Allele	A2 Case AF	A2 Control AF	p-Value
rs2588544	27113	36897513	C/T			
rs2760331	27164	36897564	C/T	0.95	0.96	0.597
rs2588543	27186	36897586	A/G	0.60	0.61	0.801
rs2588542	28341	36898741	A/T			
rs2588541	29160	36899560	C/T	0.62	0.61	0.972
rs2588540	29844	36900244	A/G	0.60	0.59	0.810
rs2760336	30665	36901065	G/T			
rs2760337	30830	36901230	A/G	0.16	0.17	0.659
rs2028732	31061	36901461	A/C	0.60	0.60	0.976
rs2588538	31523	36901923	C/T	0.61	0.61	0.912
rs1992617	32326	36902726	C/T	0.61	0.59	0.583
rs1998469	32346	36902746	A/G			
rs1998470	32358	36902758	C/T	0.84	0.81	0.338
rs1975498	34909	36905309	C/T			
rs1562093	34975	36905375	A/G	0.88	0.84	0.199
rs1975497	35066	36905466	C/T	0.13	0.15	0.613
rs1562092	35096	36905496	G/T			
rs2248788	35375	36905775	C/T	0.30	0.31	0.884
rs1899862	36304	36906704	A/G	0.17	0.18	0.563
rs2588532	36712	36907112	A/T	0.29	0.29	0.952
rs1885878	36770	36907170	C/T	0.33	0.36	0.405
rs986648	37342	36907742	C/T	0.75	0.72	0.283
rs986647	37412	36907812	C/T	0.79	0.74	0.186
rs1010010	37884	36908284	A/G	0.25	0.26	0.843
rs1010009	38077	36908477	A/C	0.25	0.24	0.764
rs2760325	38300	36908700	C/T			
rs2588531	38301	36908701	C/T			
rs1838388	41189	36911589	C/T	0.76	0.72	0.284
rs1975495	44408	36914808	C/T			
rs2181491	44493	36914893	A/C	0.12	0.15	0.464
rs1975496	44571	36914971	A/G	0.27	0.25	0.577
rs2181492	44670	36915070	A/G	0.10	0.11	0.844
rs2224719	45219	36915619	A/G	0.78	0.75	0.426
rs2224720	45258	36915658	C/T	0.21	0.20	0.790
rs1951770	47261	36917661	A/G	0.19	0.20	0.796
rs2296040	48473	36918873	A/C	0.43	0.42	0.804
rs1957723	48771	36919171	A/G	0.41	0.42	0.653
rs1957725	55292	36925692	C/T	0.77	0.75	0.439
rs2889346	56479	36926879	A/G	0.56	0.56	0.948
rs1885879	56747	36927147	A/C	0.46	0.45	0.959
rs1957726	60620	36931020	G/T	0.14	0.15	0.673
rs1957727	60688	36931088	A/C	0.76	0.73	0.255
rs1885880	61058	36931458	A/C	0.43	0.45	0.614
rs1885881	61129	36931529	C/T	0.13	0.10	0.346
rs942108	61577	36931977	C/T	0.58	0.56	0.730
rs1951771	61961	36932361	A/G			
rs2376323	63351	36933751	G/T			
rs2013358	63926	36934326	A/G	0.13	0.15	0.469
rs2181494	65798	36936198	A/G	0.46	0.47	0.820
rs1957728	66043	36936443	A/C			
rs1957729	66044	36936444	A/G	0.80	0.78	0.440
rs1957730	66246	36936646	C/T	0.15	0.17	0.668
rs1957731	66318	36936718	C/T	0.14	0.16	0.387
rs1998468	66547	36936947	G/T	0.12	0.13	0.615
rs1957732	71238	36941638	C/T	0.09	0.11	0.469
rs1957733	71283	36941683	A/G	0.60	0.02	
rs2376322	71492	36941892	A/G	0.27	0.29	0.582

dbSNP rs#	Position in SEQ ID NO: 2	Chromosome Position	A1/A2 Allele	A2 Case AF	A2 Control AF	p-Value
rs2889345	72274	36942674	A/G	0.17	0.21	0.308
rs1815267	73762	36944162	A/T	0.46	0.41	0.151
rs1957734	74209	36944609	G/T	0.68	0.69	0.766
rs1957735	75284	36945684	A/T	0.62	0.58	0.311
rs1957736	77347	36947747	A/C	0.07	0.08	0.688
rs1957737	77589	36947989	C/T	0.75	0.71	0.305
rs1957738	78096	36948496	A/G			
rs1957739	78606	36949006	A/G			
rs1957740	78862	36949262	G/T			
rs1957741	79135	36949535	A/G	0.78	0.76	0.446
rs1957742	79146	36949546	A/G	0.96	0.96	0.938
rs1957743	79456	36949856	C/T	0.17	0.19	0.667
rs1957744	79609	36950009	A/G	0.69	0.66	0.423
rs1957745	80086	36950486	A/G	0.90	0.89	0.738
rs1957746	80119	36950519	A/G	0.37	0.35	0.708
rs1957747	80766	36951166	C/T	0.72	0.70	0.639
rs2146670	81110	36951510	A/G	0.75	0.72	0.306
rs2146671	81269	36951669	A/T	0.16	0.17	0.806
rs1957748	81668	36952068	C/T	0.14	0.17	0.453
rs2162307	82433	36952833	C/T	0.76	0.73	0.465
rs1962839	82559	36952959	C/G			
rs2376315	83298	36953698	C/T	0.64	0.63	0.767
rs1426410	83821	36954221	A/G	0.77	0.74	0.465
rs1895921	84121	36954521	C/T	0.78	0.75	0.320
rs1895922	84147	36954547	C/T	0.12	0.13	0.586
rs1035779	84543	36954943	A/G	NA	0.65	NA
rs1035780	84554	36954954	A/G			
rs1035781	84691	36955091	A/G	0.75	0.76	0.830
rs1035782	84727	36955127	A/G			
rs1426411	85678	36956078	C/T	0.78	0.76	0.488
rs1834602	86699	36957099	C/T	0.18	0.18	0.945
rs1834603	86700	36957100	A/G	0.95	NA	
rs1834604	86792	36957192	A/G	0.72	0.69	0.427
rs1834605	86832	36957232	A/G	0.73	0.72	0.647
rs2162308	87045	36957445	A/G			
rs1365341	87140	36957540	A/G	0.16	0.17	0.667
rs1820458	87365	36957765	A/C	0.23	0.24	0.670
rs1469310	88342	36958742	C/T	0.19	0.21	0.592
rs3057879	88498	36958898	-/TCA	0.74	0.71	0.478
rs1469311	88589	36958989	A/G	0.74	0.72	0.582
rs768326	95502	36965902	A/G			
rs1863523	96968	36967368	C/T	0.20	0.21	0.687
rs1469312	97448	36967848	C/T	0.76	0.75	0.807
rs1469313	97568	36967968	C/T	0.78	0.79	0.824
rs1951773	98724	36969124	C/T			
rs2120655	Not mapped	Not mapped	T/G			
rs2181495	Not mapped	Not mapped	G/A			

[0237] Allelotyping results were considered particularly significant with a calculated p-value of less than or equal to 0.05 for allelotype results. These values are indicated in bold. The allelotyping p-values were plotted in Figure 1B for the discovery cohort. The position of each SNP on the chromosome is presented on the x-axis. The y-axis gives the negative logarithm (base 10) of the p-value comparing the

estimated allele in the case group to that of the control group. The minor allele frequency of the control group for each SNP designated by an X or other symbol on the graphs in Figure 1B can be determined by consulting Table 17. For example, the left-most X on the left graph is at position 36870611. By proceeding down the Table from top to bottom and across the graphs from left to right the allele frequency associated with each symbol shown can be determined.

[0238] To aid the interpretation, multiple lines have been added to the graph. The broken horizontal lines are drawn at two common significance levels, 0.05 and 0.01. The vertical broken lines are drawn every 20kb to assist in the interpretation of distances between SNPs. Two other lines are drawn to expose linear trends in the association of SNPs to the disease. The light gray line (or generally bottom-most curve) is a nonlinear smoother through the data points on the graph using a local polynomial regression method (W.S. Cleveland, E. Grosse and W.M. Shyu (1992) Local regression models. Chapter 8 of Statistical Models in S eds J.M. Chambers and T.J. Hastie, Wadsworth & Brooks/Cole). The black line provides a local test for excess statistical significance to identify regions of association. This was created by use of a 10kb sliding window with 1kb step sizes. Within each window, a chi-square goodness of fit test was applied to compare the proportion of SNPs that were significant at a test wise level of 0.01, to the proportion that would be expected by chance alone (0.05 for the methods used here). Resulting p-values that were less than 10^{-8} were truncated at that value.

[0239] Finally, the exons and introns of the genes in the covered region are plotted below each graph at the appropriate chromosomal positions. The gene boundary is indicated by the broken horizontal line. The exon positions are shown as thick, unbroken bars. An arrow is placed at the 3' end of each gene to show the direction of transcription.

Example 6 SNW1 Region Proximal SNPs

[0240] SNP rs1477261 is associated with osteoarthritis and is described in Table A. It lies within an intron of the SKI-interacting protein gene (SNW1). This gene, a member of the SNW gene family, encodes a coactivator that enhances transcription from some Pol II promoters. This coactivator can bind to the ligand-binding domain of the vitamin D receptor and to retinoid receptors to enhance vitamin D-, retinoic acid-, estrogen-, and glucocorticoid-mediated gene expression. It also can interact with poly(A)-binding protein 2 to directly control the expression of muscle-specific genes at the transcriptional level. One hundred sixty-three additional allelic variants proximal to rs1477261 were identified and subsequently allelotyped in osteoarthritis case and control sample sets as described in Examples 1 and 2. The polymorphic variants are set forth in Table 20. The chromosome position provided in column four of Table 20 is based on Genome "Build 34" of NCBI's GenBank.

TABLE 20

dbSNP rs#	Chromosome	Position in SEQ ID NO: 3	Chromosome Position	Allele Variants
rs7143926	14	218	76161268	a/t
rs1549071	14	1440	76162490	c/t
rs8012858	14	1442	76162492	c/t
rs7155611	14	2611	76163661	c/t
rs176941	14	4317	76165367	a/c
rs176942	14	4724	76165774	a/g
rs176943	14	4788	76165838	g/t
rs176944	14	5202	76166252	g/t
rs4365221	14	5780	76166830	c/t
rs3168952	14	5974	76167024	c/t
rs176945	14	6644	76167694	c/g
rs176946	14	7430	76168480	a/g
rs176947	14	7938	76168988	c/t
rs176948	14	8095	76169145	c/t
rs176949	14	8183	76169233	a/c
rs176950	14	8312	76169362	c/t
rs176951	14	8352	76169402	a/c
rs7156905	14	9348	76170398	c/t
rs3217197	14	9378	76170428	-/tctc
rs2270443	14	9617	76170667	a/g
rs176952	14	9727	76170777	c/t
rs176953	14	9834	76170884	c/t
rs176954	14	9899	76170949	g/t
rs176955	14	10211	76171261	c/t
rs3214416	14	10377	76171427	-/t
rs176956	14	10695	76171745	c/t
rs2544566	14	10729	76171779	c/g
rs2544567	14	10730	76171780	c/t
rs176957	14	11433	76172483	a/g
rs176958	14	11951	76173001	c/g
rs176959	14	12697	76173747	c/t
rs1802227	14	12982	76174032	a/c
rs176961	14	14419	76175469	c/t
rs176962	14	14501	76175551	c/t
rs7401285	14	14983	76176033	a/c
rs176963	14	15280	76176330	c/t
rs176964	14	15475	76176525	a/g
rs4903631	14	15888	76176938	a/g
rs4903632	14	15976	76177026	a/t
rs176965	14	16307	76177357	a/c
rs4903633	14	16442	76177492	a/c
rs176966	14	17255	76178305	c/t
rs176968	14	18948	76179998	g/t
rs176969	14	19435	76180485	a/t
rs176970	14	19753	76180803	c/t
rs7149198	14	20021	76181071	c/t

dbSNP rs#	Chromosome	Position in SEQ ID NO: 3	Chromosome Position	Allele Variants
rs7147918	14	20022	76181072	a/c
rs7148685	14	20503	76181553	a/g
rs1184232	14	20590	76181640	g/t
rs1184233	14	21804	76182854	g/t
rs1184234	14	21919	76182969	c/t
rs7401998	14	21990	76183040	a/t
rs176974	14	22412	76183462	a/g
rs6574390	14	22536	76183586	c/t
rs176975	14	23432	76184482	a/g
rs176976	14	23468	76184518	g/t
rs176977	14	23772	76184822	c/t
rs8013727	14	24325	76185375	c/t
rs176978	14	24773	76185823	c/t
rs2111829	14	26274	76187324	c/t
rs176980	14	27440	76188490	c/g
rs5809848	14	28561	76189611	-/acag
rs5809849	14	30071	76191121	-/a
rs4383070	14	31764	76192814	a/t
rs7493652	14	33008	76194058	c/t
rs2112133	14	35310	76196360	a/t
rs1963833	14	35460	76196510	a/c
rs6574391	14	37112	76198162	a/g
rs7155062	14	37285	76198335	a/g
rs4899674	14	37747	76198797	c/t
rs8022516	14	38057	76199107	c/t
rs7140838	14	38859	76199909	a/c
rs7141127	14	38860	76199910	a/g
rs6574392	14	39525	76200575	a/g
rs8003691	14	40216	76201266	a/g
rs8003979	14	40281	76201331	c/t
rs8010541	14	41453	76202503	c/g
rs8016416	14	42091	76203141	a/t
rs8016175	14	42513	76203563	a/g
rs7154571	14	42935	76203985	c/t
rs7158826	14	42985	76204035	a/g
rs7159310	14	43003	76204053	a/g
rs7401900	14	43281	76204331	a/g
rs7160355	14	43716	76204766	c/t
rs2032781	14	43866	76204916	a/g
rs6574394	14	44234	76205284	g/t
rs8007598	14	44596	76205646	a/g
rs2267767	14	44871	76205921	c/t
rs6574395	14	45005	76206055	a/g
rs7150066	14	45282	76206332	a/c
rs7492334	14	47178	76208228	a/c
rs4359361	14	47816	76208866	g/t
rs4605089	14	47887	76208937	a/g

dbSNP rs#	Chromosome	Position in SEQ ID NO: 3	Chromosome Position	Allele Variants
rs7146446	14	48134	76209184	c/t
rs4346144	14	48135	76209185	a/g
rs7148078	14	48276	76209326	g/t
rs7148286	14	48400	76209450	c/t
rs3783980	14	48798	76209848	a/g
rs1549119	14	48803	76209853	a/t
rs1984925	14	49146	76210196	c/t
rs1477261	14	49969	76211019	a/t
rs8016447	14	51059	76212109	a/g
rs7494044	14	51064	76212114	c/t
rs2023288	14	53285	76214335	a/t
rs7151685	14	54560	76215610	c/t
rs2112135	14	54748	76215798	a/g
rs2161088	14	54785	76215835	c/g
rs4903638	14	55102	76216152	c/g
rs1477262	14	55644	76216694	a/g
rs1477263	14	55705	76216755	g/t
rs1477264	14	55841	76216891	a/g
rs2277917	14	56623	76217673	c/g
rs2277918	14	56825	76217875	a/c
rs2277919	14	56827	76217877	a/g
rs1978416	14	56892	76217942	c/t
rs3759728	14	59150	76220200	a/t
rs6574399	14	59958	76221008	a/t
rs7155336	14	60231	76221281	c/t
rs7156186	14	60524	76221574	a/g
rs7142390	14	61871	76222921	c/t
rs7145875	14	62226	76223276	c/t
rs8014635	14	63230	76224280	g/t
rs8015938	14	63468	76224518	g/t
rs8015313	14	63787	76224837	c/t
rs8006315	14	65732	76226782	a/c
rs6574400	14	65989	76227039	a/g
rs7140816	14	68832	76229882	g/t
rs4566078	14	69904	76230954	c/t
rs7141050	14	70365	76231415	a/g
rs3049356	14	70886	76231936	-/tatc
rs4903639	14	73088	76234138	a/t
rs4903641	14	73103	76234153	c/t
rs2364838	14	75934	76236984	c/t
rs2364839	14	75966	76237016	c/t
rs4632066	14	76273	76237323	c/t
rs2112136	14	77943	76238993	c/t
rs4641655	14	78466	76239516	c/t
rs4635269	14	78861	76239911	c/t
rs4570764	14	78872	76239922	a/g
rs759808	14	79836	76240886	g/t

dbSNP rs#	Chromosome	Position in SEQ ID NO: 3	Chromosome Position	Allele Variants
rs7150531	14	80908	76241958	c/t
rs7154968	14	81509	76242559	c/g
rs7146657	14	83576	76244626	c/t
rs7145859	14	83662	76244712	c/g
rs4903643	14	83782	76244832	c/t
rs717682	14	84282	76245332	g/t
rs717683	14	84444	76245494	a/g
rs1477259	14	85129	76246179	c/g
rs8019064	14	85151	76246201	a/g
rs8018971	14	85296	76246346	a/c
rs1477260	14	85809	76246859	c/g
rs5809851	14	86387	76247437	-/t
rs1985149	14	86494	76247544	a/g
rs1008988	14	89786	76250836	a/g
rs1008989	14	89894	76250944	a/t
rs8018222	14	90122	76251172	g/t
rs1006040	14	92067	76253117	a/g
rs1006039	14	92187	76253237	c/t
rs1006038	14	92312	76253362	a/g
rs8009784	14	92824	76253874	g/t
rs4903644	14	93733	76254783	c/t
rs7149496	14	96553	76257603	c/g
rs6574402	14	96941	76257991	a/c

Assay for Verifying and Allelotyping SNPs

[0241] The methods used to verify and allelotype the 101 proximal SNPs of Table 20 are the same methods described in Examples 1 and 2 herein. The primers and probes used in these assays are provided in Table 21 and Table 22, respectively.

TABLE 21

dbSNP rs#	Forward PCR primer	Reverse PCR primer
rs7143926	ACGTTGGATGGAGTCACCCAAAATTAAGGC	ACGTTGGATGGAAAGCCAAAATTAGCCTGC
rs1549071	ACGTTGGATGGTGAGACGCTGTCTCAGTAA	ACGTTGGATGCTCCACACTTGGAGAAGTTG
rs8012858	ACGTTGGATGGTGAGACGCTGTCTCAGTAA	ACGTTGGATGCTCCACACTTGGAGAAGTTG
rs7155611	ACGTTGGATGATGGAATACAGGCACCGTTC	ACGTTGGATGCCCTTCTTAATCTCCATGG
rs176941	ACGTTGGATGTTAGTATGGGAAAAGGGCTC	ACGTTGGATGCAACAATCCTATGAGTTGGG
rs176942	ACGTTGGATGAGTGGCTCAGATGTGAGTAG	ACGTTGGATGTGGTCTTCACCAACCACATG
rs176943	ACGTTGGATGACCAAGCCAGTAAAGTCTC	ACGTTGGATGGCATCCGCAAGATGCTAATG
rs176944	ACGTTGGATGGGCCTCAATATTGGCTAAATG	ACGTTGGATGCTTAACCATTAGAGCCCTTC
rs4365221	ACGTTGGATGAAATAAGGCAGGAAGGGTAG	ACGTTGGATGTCCCAACTTACTGGTCTTTC
rs3168952	ACGTTGGATGATGTACCAGACTTGGTGGTG	ACGTTGGATGTTTGCTGAGGATGGAGACTG
rs176945	ACGTTGGATGCCTACTATACACTCACAAA	ACGTTGGATGTTTTTAAACACTTTAAGC

dbSNP rs#	Forward PCR primer	Reverse PCR primer
rs176946	ACGTTGGATGGCTTTATCATAGGTATTTGTG	ACGTTGGATGGAGAGATGTGTTGTTTTGAG
rs176947	ACGTTGGATGTGAGTAGCTGGGACTACAGG	ACGTTGGATGGGCCAACATAGCGAACTCC
rs176948	ACGTTGGATGCAGAGCCAAAGGTCAACAAG	ACGTTGGATGTACAGGTGTGAGCCTTCATG
rs176949	ACGTTGGATGTAGGAACTCCCTGCAGTTCC	ACGTTGGATGCCTTGCTGGCTTTAAAGAAG
rs176950	ACGTTGGATGAATCACAGGAGTGACATCCC	ACGTTGGATGTGGAGGAGAAACCTGACTTG
rs176951	ACGTTGGATGCCCTATATAATCTCCTCCCC	ACGTTGGATGCAGGAGTGACATCCCATTAC
rs7156905	ACGTTGGATGTGAGAGAGAGAACTGTCTC	ACGTTGGATGAAAGGCGGCTTTGATGTTGG
rs3217197	ACGTTGGATGTTGATTGTGCCACTGCACTC	ACGTTGGATGACTCTAGTTGAAAATCCTGG
rs2270443	ACGTTGGATGATAACTCAGTCCAGGTGTGG	ACGTTGGATGCACTCAAGCAGTCTACTCAC
rs176952	ACGTTGGATGGATCTCAGCTCACTGCAATC	ACGTTGGATGTATCTGGGTGACTGAGGAAG
rs176953	ACGTTGGATGTTGAGGTCAGGAGTTTGGGA	ACGTTGGATGGCCACCACACCCAGCTAATT
rs176954	ACGTTGGATGAAAACATAGGCCAGGTGCAG	ACGTTGGATGAAACTCCTGACCTCAAGCCA
rs176955	ACGTTGGATGCTAGAGTGCTTGGATGTACC	ACGTTGGATGGTCATCTACAGGGACTAGAC
rs3214416	ACGTTGGATGACGACTATCATCACGTGTTT	ACGTTGGATGACCAGAAGTCTGTAAGTAGG
rs176956	ACGTTGGATGTACAGGCATAAGCCACCATG	ACGTTGGATGAGGAAGGGTGTAAGCAAGG
rs2544566	ACGTTGGATGCAAGCAATCTTCCCATCTGG	ACGTTGGATGTGATCCGATTTTTGGCTGGG
rs2544567	ACGTTGGATGCAAGCAATCTTCCCATCTGG	ACGTTGGATGTGATCCGATTTTTGGCTGGG
rs176957	ACGTTGGATGTTTCACCGTGTAGCCAGGA	ACGTTGGATGTAATCCAGCACTTTGGGAG
rs176958	ACGTTGGATGAAAACCTGGGCACTCTACCAC	ACGTTGGATGAAAATCGCGCCATTGCACTC
rs176959	ACGTTGGATGCAGGCAGTTTTTATTTGTCCC	ACGTTGGATGGGTTAGGAGTCATAATACC
rs1802227	ACGTTGGATGAACAAATAGTTGCACCAAG	ACGTTGGATGTTTTAATTTGGAGTGGGCA
rs176961	ACGTTGGATGAACCCAGTTTAAGACCGGCC	ACGTTGGATGTACAGGTGTGTGCCACCATG
rs176962	ACGTTGGATGATATTTCTGGCTGGGCACTG	ACGTTGGATGACTGGGTCAAGCAATCTGC
rs7401285	ACGTTGGATGACAGAGTGGGACTCCATATC	ACGTTGGATGGATTCAAACCTGGGTGTCTTG
rs176963	ACGTTGGATGTAAGCCTGGGAAAACACACG	ACGTTGGATGCCCACTCTACTTTCCAGTAG
rs176964	ACGTTGGATGAGAGTCAGTGTCTACAAAA	ACGTTGGATGTAATCCCGTTTTACAGCTTC
rs4903631	ACGTTGGATGGTAAATGCCAGCATGATGAC	ACGTTGGATGTCTCAGCCCACTATAAGAAG
rs4903632	ACGTTGGATGTGTGAATACCTATCCTCAGG	ACGTTGGATGGTCATCATGCTGGCATTAC
rs176965	ACGTTGGATGAATGCTTTATAAGGGCTGCC	ACGTTGGATGTCTCAGAAACAAAGGATGTG
rs4903633	ACGTTGGATGCAACCCCCAAACCATCATAT	ACGTTGGATGCTAACAGATTCTGTTGACATGG
rs176966	ACGTTGGATGCTCTCGAGTAGCTGGGACTA	ACGTTGGATGTGGCCAACATGGTGAAACCC
rs176968	ACGTTGGATGGCGAAACTCCGTCTCAAAAC	ACGTTGGATGTAGTGATCTTCCACCTAGG
rs176969	ACGTTGGATGCTGTCTGTCCGATTACTGC	ACGTTGGATGTCTAGAATCAAGCATGCGGC
rs176970	ACGTTGGATGCTAATGTTTCTAGTACAGTGG	ACGTTGGATGCTTCTCTTCTAGCTATTTTGC
rs7149198	ACGTTGGATGCAATGGGATATTACTCAGCC	ACGTTGGATGTTTCTGTGCCGGGCTTATTC
rs7147918	ACGTTGGATGCAATGGGATATTACTCAGCC	ACGTTGGATGTTTCTGTGCCGGGCTTATTC
rs7148685	ACGTTGGATGTGTCTTCTTTTGGAGCCGTC	ACGTTGGATGCTCAATCGAAAGAAACGAG
rs1184232	ACGTTGGATGAAGAGGCCACCTACAGAATG	ACGTTGGATGCTCGTTTCTTTGCGATTGAG
rs1184233	ACGTTGGATGAAGTGTGGGATTACAGGTG	ACGTTGGATGAGTGAAAGATCGCCACAAAG
rs1184234	ACGTTGGATGGCTATGTGCAGTCACTCATG	ACGTTGGATGTCTCAGACCTCAGGTGATCT
rs7401998	ACGTTGGATGTGAGTAGCTAGGACAACAGG	ACGTTGGATGAACGTGGTGAAACCCCATCT
rs176974	ACGTTGGATGTTACAGCGAGCTGAGATCAT	ACGTTGGATGAGGATCATACTGTCTCTGAC
rs6574390	ACGTTGGATGTGATGAAACCCCGTCTGTAC	ACGTTGGATGTCCTGAGTAGCTGGGATTAC
rs176975	ACGTTGGATGTGTAGAATCTAGGTGGTAGG	ACGTTGGATGCCAGCCTTTCTGACATTTT
rs176976	ACGTTGGATGGGTAGGAGATACAGGTGTTT	ACGTTGGATGCCAGCCTTTCTGACATTTT
rs176977	ACGTTGGATGTTGCATCATTACACTTCAGC	ACGTTGGATGGGGAAACATTATGCATAATTCC
rs8013727	ACGTTGGATGTGCCTGGTTGTATACCTAAC	ACGTTGGATGCTTGAGAACGATTCTGTTGTC

dbSNP rs#	Forward PCR primer	Reverse PCR primer
rs176978	ACGTTGGATGGGGACCATGTTTTGTTACC	ACGTTGGATGAATACTGTGGAATGGGCATG
rs2111829	ACGTTGGATGCATGTGGAAAAAGGTATGAC	ACGTTGGATGCCTACTTTATATGCAGTAGG
rs176980	ACGTTGGATGATGGCCAATGCTATGAACGC	ACGTTGGATGAAGGGCAGTTGCAGGAAAAAG
rs5809848	ACGTTGGATGTCTATTTTTCCAGAGCTTGGG	ACGTTGGATGCCATTTCACTGATGCTTTGG
rs5809849	ACGTTGGATGGTGAATACCGTGTCAGTTCC	ACGTTGGATGTGCAGTGAGCTGAGATCATG
rs4383070	ACGTTGGATGAGCGATTCTCTTGTCTCAGC	ACGTTGGATGAACTTAGCTGGGCATTGTGG
rs7493652	ACGTTGGATGGGTCAATATACCACAAGTAAC	ACGTTGGATGCTGGCCCTATGCTATTTTCA
rs2112133	ACGTTGGATGGCCACCACAAGTGGCTAATT	ACGTTGGATGTGTGGTCAGGAGATCGAAAC
rs1963833	ACGTTGGATGTAAGCCAAGATTGCGTCACT	ACGTTGGATGAGCATTAAAGGTAGAATGCC
rs6574391	ACGTTGGATGTAACCGTTGCTATGGAGAAG	ACGTTGGATGACCTATACAACCCTAAGCTG
rs7155062	ACGTTGGATGGCTCCTTATTTGGGCATTCC	ACGTTGGATGCACTCAGCCTTGTGAGATAC
rs4899674	ACGTTGGATGAATGTGCTGAGGAACTGAG	ACGTTGGATGGCTTCTGATACTTTCAAGAG
rs8022516	ACGTTGGATGGTTGAAGGCATTCTTTTGGG	ACGTTGGATGCTAGCCTGGGCAATATAATG
rs7140838	ACGTTGGATGCCTCGTTTCTGAAGAATACC	ACGTTGGATGGAGACTGAACAGGTTATTGG
rs7141127	ACGTTGGATGCCTCGTTTCTGAAGAATACC	ACGTTGGATGGAGACTGAACAGGTTATTGG
rs6574392	ACGTTGGATGAGAAAATAGCATAGGCTGGG	ACGTTGGATGAAATGATCCATCCTCCTCAG
rs8003691	ACGTTGGATGACTGAAGTCAAGTGAAGGCC	ACGTTGGATGTTAGGCCCTATACATGGAG
rs8003979	ACGTTGGATGCACAAAACCACTTCTGAAGC	ACGTTGGATGGGGCCTAATTTTCTTTTGC
rs8010541	ACGTTGGATGCACTTTTCTTGGCTAGCTTC	ACGTTGGATGCAGAATGGCTAAAACCTGAAC
rs8016416	ACGTTGGATGTGCCATAACTTCCTTTGAC	ACGTTGGATGGCCACGGAATCCTATATAGA
rs8016175	ACGTTGGATGTTGAGCACTGAGTGAGTGAG	ACGTTGGATGTCCTAACCGTGAGTGATCTG
rs7154571	ACGTTGGATGATGTGAGGAGCACCTCTGCC	ACGTTGGATGCTCTTCCCTTCTCAGACGG
rs7158826	ACGTTGGATGCACCTCCCTCCTGGACGGG	ACGTTGGATGGCCACCCCGTCTGAGAAGG
rs7159310	ACGTTGGATGACCCCGTCTGAGAAGGGAAG	ACGTTGGATGCACCTCCCTCCTGGACGGG
rs7401900	ACGTTGGATGCCCAACAGCTCATTGAGAAC	ACGTTGGATGTCTTTTCCCACATTTCCCC
rs7160355	ACGTTGGATGTCACTTGTTTATCTGCTGAC	ACGTTGGATGTTATTGATCATTCTTGGGTG
rs2032781	ACGTTGGATGTATATCACTGTAGTAACAGC	ACGTTGGATGACCATAAGTATATATCACAAG
rs6574394	ACGTTGGATGACCACACCCAGCCTATTTGT	ACGTTGGATGTTATGCTGAAAGCCTGGGAG
rs8007598	ACGTTGGATGCTGGCAAAAGTCTCTTAACAC	ACGTTGGATGTTGGTTAAAGTCACAGAATG
rs2267767	ACGTTGGATGGTTTCACCATGTTAGCCAGG	ACGTTGGATGTAATCCCAGCACTTTGGGAG
rs6574395	ACGTTGGATGAACCTTGAACCTTGGGCTC	ACGTTGGATGAAAAAATTCACCGGGCATGG
rs7150066	ACGTTGGATGAAGCAATCCTCCTGCTTCTG	ACGTTGGATGAGATCAGGTGTAGATCCAGG
rs7492334	ACGTTGGATGGCCTTTGCATTGGCTATTTG	ACGTTGGATGTAGAAAGCAGTCATGGGAAG
rs4359361	ACGTTGGATGGTAGTATTTGCTTAGTACAC	ACGTTGGATGTTCTAAGCCTGAATGTTTCC
rs4605089	ACGTTGGATGAATACCTATGAGATCTCAGG	ACGTTGGATGCCTTGTAACCTCTTAAACATC
rs7146446	ACGTTGGATGATTCACCTTTTACAAGACCTC	ACGTTGGATGGCATATTGTACTTAGGAACTC
rs4346144	ACGTTGGATGATTCACCTTTTACAAGACCTC	ACGTTGGATGGCATATTGTACTTAGGAACTC
rs7148078	ACGTTGGATGTGTGTCAGATTGATGGCTTG	ACGTTGGATGCCAAGAGAATAAAGCTGAGAG
rs7148286	ACGTTGGATGGTGGTCATTAAGCTTGCCAG	ACGTTGGATGTGCTATGGATGCTGCTTGAG
rs3783980	ACGTTGGATGTTTTTGGCCAGGTAAGAC	ACGTTGGATGTGGTGCTTTTGTCTCTCTG
rs1549119	ACGTTGGATGTTTCATCTTCTCTGCCTCC	ACGTTGGATGGTGAAGGCCAGTCATATTGC
rs1984925	ACGTTGGATGAAGTAGCCAGGATTACAGGC	ACGTTGGATGCCAGCCTAGCAAACATGGTG
rs1477261	ACGTTGGATGCAGGGTTATGTGGTATTATC	ACGTTGGATGGGGAAAAGTAAAAGATAAGAG
rs8016447	ACGTTGGATGAATTACAGACGTGTGCCACC	ACGTTGGATGTGACACAGAGAGACTCTGTC
rs7494044	ACGTTGGATGAATTACAGACGTGTGCCACC	ACGTTGGATGTGACACAGAGAGACTCTGTC
rs2023288	ACGTTGGATGGAGAAAAATTGTGATTGATTG	ACGTTGGATGGCCATCAAATCAATCTAATC
rs7151685	ACGTTGGATGACAGTGCTGGCATTACTGGC	ACGTTGGATGTAAAGATCGTCTGCCACTGC

dbSNP rs#	Forward PCR primer	Reverse PCR primer
rs2112135	ACGTTGGATGAGTGCAGTGGCCCAATCACA	ACGTTGGATGGTCTAGAGTCCCAGCTACTC
rs2161088	ACGTTGGATGTATAGGGTCTCACTCTTGCC	ACGTTGGATGAGGAGGATCACCTGAGCCTT
rs4903638	ACGTTGGATGATAGGGTGTACTGCGTTGG	ACGTTGGATGAGGCCTAGGTGAGAAGATTG
rs1477262	ACGTTGGATGATGCGTGAGGAGAATGAAGG	ACGTTGGATGAAGGCTAGTGTTCAAGGAAGG
rs1477263	ACGTTGGATGAACCTTCCTGAACACTAGCC	ACGTTGGATGCCTTGCTGCCCATTTTAAG
rs1477264	ACGTTGGATGCGTAGATAGAACCACCTCAG	ACGTTGGATGAAAGGCGGAGAGCACTTTAC
rs2277917	ACGTTGGATGGCATTGTGCTAGCTGAAG	ACGTTGGATGTTGAACAGGAGTACCGTTTG
rs2277918	ACGTTGGATGTTACGTTCTTACTCAGTCC	ACGTTGGATGACCTGTCTGTTTTAAACGCC
rs2277919	ACGTTGGATGTTACGTTCTTACTCAGTCC	ACGTTGGATGACCTGTCTGTTTTAAACGCC
rs1978416	ACGTTGGATGAGGGCGTTTAAACGACAGG	ACGTTGGATGCGGGTGAGAGGATATGTTT
rs3759728	ACGTTGGATGATAGTCCCTCGCTGTTTTGG	ACGTTGGATGAGAAAGCACTAGGCCTTTGG
rs6574399	ACGTTGGATGATGCTCTGATGCCATTATGC	ACGTTGGATGAGGGCACGTAACACATCC
rs7155336	ACGTTGGATGGAGGAAGACTCGGTCTAAA	ACGTTGGATGAACAATCTGACACTAGGTGC
rs7156186	ACGTTGGATGATTACGGGTATGAGCCACTG	ACGTTGGATGGAAGTGGACATTAGGTCTGG
rs7142390	ACGTTGGATGTAATCAAGACAGTGTGGTAC	ACGTTGGATGGGGTTTATTTCAAGACTCTC
rs7145875	ACGTTGGATGGTCCTTTGAAGCACAAAACC	ACGTTGGATGCTTCATGATCTTGGATTTGGC
rs8014635	ACGTTGGATGGTCTTCTCACTCAAGAACAC	ACGTTGGATGCAACAGAGCAAGACTCCAAC
rs8015938	ACGTTGGATGCCCTGAACTCAAGTGATCTG	ACGTTGGATGATCTAAACAGTGTTCTGGC
rs8015313	ACGTTGGATGAAACTGATTCTGTACCTGG	ACGTTGGATGGTCAGTCATTTTATAGGCAG
rs8006315	ACGTTGGATGTCACCTGAGGTCAGGAGTTC	ACGTTGGATGCCATGCCTGGCTAAGTTTG
rs6574400	ACGTTGGATGTTATCCTTCTCTGCCAGTG	ACGTTGGATGCCTTTGAACTTCTACCCAG
rs7140816	ACGTTGGATGCAATAGAGTGAGACTCTGTC	ACGTTGGATGATTGATGAGCCTCTCTTTAC
rs4566078	ACGTTGGATGTAGAGTCTTGTCTGTACC	ACGTTGGATGAGGAGAATCGCTTGAACCCA
rs7141050	ACGTTGGATGATATGTTATACATATTAGTC	ACGTTGGATGCAAGTTAACCATTATCAACTC
rs3049356	ACGTTGGATGTACCACTGGCAGAGTAGAAG	ACGTTGGATGCACATGGTTTGGGTAAGT
rs4903639	ACGTTGGATGAGCGAGACTCCGTCTCAAAA	ACGTTGGATGTCAAAGGTAGCCTTGACTGG
rs4903641	ACGTTGGATGACTCCAACCTGGGCAACAGA	ACGTTGGATGCTGGCTCCAGCACACTTATC
rs2364838	ACGTTGGATGTGTAGTCCAGCTACTTGTG	ACGTTGGATGTGATCATAGCTCACTGCAGC
rs2364839	ACGTTGGATGTGGGCAACATAGCAAGATCC	ACGTTGGATGCTCACAAGTAGCTGGGACTA
rs4632066	ACGTTGGATGGAGAAAAAAGAGATGGAGGG	ACGTTGGATGGCCCTGACTGTGTTTTATG
rs2112136	ACGTTGGATGTTTCTTGGGGACTAAGGCTC	ACGTTGGATGTAACAGGCCCTGAAGGAATG
rs4641655	ACGTTGGATGCGATAGAGCAACCCTGTCTC	ACGTTGGATGGCCCTACACCCAGATTCAAG
rs4635269	ACGTTGGATGAAAGTGCTGGGATTACAGGC	ACGTTGGATGCTTGACATATTTCTGAGG
rs4570764	ACGTTGGATGCTTGACGATATTTCTGAGG	ACGTTGGATGAAAGTGCTGGGATTACAGGC
rs759808	ACGTTGGATGATGAGCTGTGATCATGCCAC	ACGTTGGATGCCTGAACTTCATTGTGCTCC
rs7150531	ACGTTGGATGATGTGCGGTGTGAAGCAAAG	ACGTTGGATGTTGTTTGGCCTGGTCTGATG
rs7154968	ACGTTGGATGTACCCAGGTAACAAACCTGC	ACGTTGGATGTCCCCTATAAGGCTTTCAGG
rs7146657	ACGTTGGATGTGAGTAGCTGGGACTACAGG	ACGTTGGATGTAACACGGTGAAACCCCGTC
rs7145859	ACGTTGGATGAGGCAGGAGAATGGCGTGAA	ACGTTGGATGTTTTGAGACGGAGTCTTGC
rs4903643	ACGTTGGATGTATTCCATGCTGTCTGCCTC	ACGTTGGATGAGTTGACCTTAAAGGCTGGG
rs717682	ACGTTGGATGTTTAGGGACAGAGGCTGAGG	ACGTTGGATGAAGTGCAGTGGCCTGATCTC
rs717683	ACGTTGGATGTTGGCAAAAAAGGTGGAGGC	ACGTTGGATGTGATGATGGCACAGGGAATG
rs1477259	ACGTTGGATGTGACTGAGACTACCTTCACC	ACGTTGGATGAAGTGCTCACGTAGGTTGTC
rs8019064	ACGTTGGATGCCTTGACAGCAAACTTCAGAG	ACGTTGGATGTGACTGAGACTACCTTCACC
rs8018971	ACGTTGGATGATGGTCTCACTCTGTCACTC	ACGTTGGATGAATTGTTTGAGCCCAGGAGG
rs1477260	ACGTTGGATGAGTGTGATGTTAGCAAGGAC	ACGTTGGATGTGCCATCTGTTTCCCATAGG
rs5809851	ACGTTGGATGACAGAGAGTGTTCAAGCAG	ACGTTGGATGTTGGGCAACAGAGAGAGACT

dbSNP rs#	Forward PCR primer	Reverse PCR primer
rs1985149	ACGTTGGATGACTGAAATCTTTGCCTCCCG	ACGTTGGATGGTGGTGCACCTTATGTAGTCC
rs1008988	ACGTTGGATGAGTGTGTCTCAGGGAATGTG	ACGTTGGATGCCTGGCAATTTGTTCTCTGC
rs1008989	ACGTTGGATGGGAATAGCAAGTGTAAACGGC	ACGTTGGATGACTCCAACCGCATCAGCTTC
rs8018222	ACGTTGGATGATCCTCCATATGCTGAACGC	ACGTTGGATGAAGGTGGAACGAGAGACTTG
rs1006040	ACGTTGGATGTTTAGCTCTCTCTCTGTTGC	ACGTTGGATGTCTTGAGCCCAGGAGTTCAA
rs1006039	ACGTTGGATGTGAAGCTGGGAGTTAGAGAC	ACGTTGGATGCCACCATGCCCAGCTAATTT
rs1006038	ACGTTGGATGATAAGCCACTGTGCTCAGTC	ACGTTGGATGGGTAGGGTTTATTAAGTGCC
rs8009784	ACGTTGGATGTGTTTTGGCTATGCTTTGCC	ACGTTGGATGTGACAGAGCGAGACTTTGTC
rs4903644	ACGTTGGATGTTGCAGTGAGCTGAGATTGG	ACGTTGGATGGTGAATGAATGAATAAGGGCC
rs7149496	ACGTTGGATGACAACACACAGTACTGGACC	ACGTTGGATGTGGGTGCATGTTAGAAACGC
rs6574402	ACGTTGGATGCAGGTCCTTTGTCTGACAAG	ACGTTGGATGGGGATGTGCGATTTGATCTG

TABLE 22

dbSNP rs#	Extend Primer	Term Mix
rs7143926	ACCCAAAATTAAGGCAAAATGG	CGT
rs1549071	CACACACATATATACACACACA	ACG
rs8012858	CACACATATATACACACACACA	ACG
rs7155611	GGCACCGTTCTCTCTCTCA	ACT
rs176941	CTGGGCCTCAGTTTACTCAT	CGT
rs176942	AATAGGTTGGTTTGTGCCCC	ACT
rs176943	CCCGTAGTCCCTGTGAAAC	ACT
rs176944	AAAAGTCCACTAATCCTTCCAA	CGT
rs4365221	GAGGGCAACTCAACACATTTTA	ACG
rs3168952	TTGGTGGTGAGATGGACAGA	ACT
rs176945	TACTATACACTCACAAAAATTGTT	ACT
rs176946	TTGTATAACAAAATACCACAAGC	ACT
rs176947	GGCGCCCGCCACTACGC	ACG
rs176948	AAAACAGACCTCAGTCTTACA	ACT
rs176949	CTCCCTGCAGTTCCTTGTTA	CGT
rs176950	GGAGTGACATCCCATTACTTT	ACG
rs176951	TCCTCCCCTCCTTGGGTG	ACT
rs7156905	CTGTCTCAAAAAAGGAACCAG	ACT
rs3217197	CTCCAGCCTGAGTGAGAGA	ACT
rs2270443	CAGGTGTGGTGGCTCATGC	ACG
rs176952	CACTGCAATCGCTGCCTCC	ACG
rs176953	GGACCAGCCTGGCCAAACAT	ACT
rs176954	GCAGTGGCTCAATCCCAGC	CGT
rs176955	CTGCCCCCTCCAGCCCTTC	ACT
rs3214416	CATCACGTGTTCTAATGAAAA	CGT
rs176956	AAGCCACCATGCCCAGCC	ACT
rs2544566	CATCTGGGCCTCCCAAAGTA	ACT
rs2544567	CATCTGGGCCTCCCAAAGT	ACT

dbSNP rs#	Extend Primer	Term Mix
rs176957	GGTCTCGATCTCCTGACCT	ACG
rs176958	GGAGTTTTGCTCTTGTGTC	ACT
rs176959	TTTTATTTGTCCCTTGTCTTTC	ACT
rs1802227	AATAGTTGCACCAAGCAAGAG	ACT
rs176961	TATGGCAAACCCCTGTCTACA	ACT
rs176962	GGCTCACGCCTGTAATCCTA	ACT
rs7401285	GGGACTCCATATCAGAAAACA	CGT
rs176963	GAAAACACACGCGGGCGC	ACT
rs176964	CAGTGTCTACAAAAGTGCCT	ACG
rs4903631	CTTGAGACAAGATGAAACAGTT	ACG
rs4903632	ATCCTCAGGGAAACGAAAATTA	CGT
rs176965	ATAAGGGCTGCCAGCTTGAT	ACT
rs4903633	TAGCAATTTTATATCTCAGCATG	ACT
rs176966	ACCACACCCAGCTAATTTTTG	ACG
rs176968	TCACACCTGTGACTCCAGC	CGT
rs176969	CCGATTTACTGCATTGCATTTTC	CGT
rs176970	GTACAGTGGGGTGAATAGTTA	ACT
rs7149198	GATATTACTCAGCCATAAAAAAG	ACT
rs7147918	GGATATTACTCAGCCATAAAAAA	ACT
rs7148685	TTGAGACCGTCTATTCAGATC	ACT
rs1184232	GAATGGAAGAAAATGGTTGCAA	CGT
rs1184233	TGCCCAGCCTCTTCAATTAC	ACT
rs1184234	TACCAGCACTTTGGGAGGC	ACG
rs7401998	CCACGCCTGGCTAATTTTTTTT	CGT
rs176974	CTGGGCAACAAAGCAAGACT	ACG
rs6574390	AAATTAGCTGGGTATGATGGC	ACT
rs176975	AATCTAGGTGGTAGGAGATAC	ACT
rs176976	TATAATTCTTTCAGCTTTTCTGTA	ACT
rs176977	TCAGCCTGGGCAACAAGAG	ACG
rs8013727	CCTAACCATAGAAGATAATTAGAA	ACT
rs176978	ATGTTTTGTACCTCTTGTTAC	ACG
rs2111829	GAATTTTGCTTGGTGAACAAAAT	ACT
rs176980	GCTATGAACGCCATTTTATGTA	ACT
rs5809848	TGGGTCTGAAATCCTGCTG	CGT
rs5809849	CGTGTCAAGTCCTTTTTTTTTT	ACT
rs4383070	GCCTCCTGAGTAGCTGGG	CGT
rs7493652	TATACCACAAGTAAGTGTAAATT	ACG
rs2112133	CCACAAGTGGCTAATTTTTTGT	CGT
rs1963833	CTGGGTGACAGAGCAAGAC	CGT
rs6574391	TGGAGAAGTGATAAACTC	ACG
rs7155062	ATAACCCTTCAAATGAGCATCA	ACT
rs4899674	GGCAAATGGGCTGGGGAG	ACG
rs8022516	AGGCATTCTTTTGGGTATAGTA	ACG
rs7140838	TCTGAAGAATACCAGACCTCT	CGT

dbSNP rs#	Extend Primer	Term Mix
rs7141127	CTGAAGAATACCAGACCTCTC	ACT
rs6574392	CTGGGCACAGCGACTCAC	ACT
rs8003691	TGAAGGCCTCCATGGTATAG	ACT
rs8003979	TCTGAAGCCAGTGAGGAAGT	ACT
rs8010541	GCTAGCTTCAACTCTCCTGAT	ACT
rs8016416	TAACCTTCCTTTGACTTGCTTTTT	CGT
rs8016175	GTCTGCAATCCCGGCACCT	ACG
rs7154571	GTGAGGAGCGTCTCTGCC	ACG
rs7158826	TCGCTCCTCACTTCCCAGA	ACG
rs7159310	CATCTGGGAAGTGAGGAGC	ACT
rs7401900	TGAGAACAGGCCATGATGAC	ACT
rs7160355	CCTGCCAAATCCCCCTCTC	ACG
rs2032781	GAGAAAAGCGGGCAGGACT	ACT
rs6574394	CACCCAGCCTATTTGTATAATT	ACT
rs8007598	CTCTTAACACATTTTTTTACAGCA	ACG
rs2267767	CTGACCTCGTGATCTGCCC	ACT
rs6574395	GGCTCAGGCGATCATCGTA	ACG
rs7150066	CTGCCACCCAAAGTGCTGG	ACT
rs7492334	TTGTGTGTGTGTGTGTGTGG	ACT
rs4359361	GCTTAGTACACTTTAAACATGAT	ACT
rs4605089	TCAGGAACACCGCTTAATTTTT	ACG
rs7146446	CAAGACCTCTTTAAGTAATACTC	ACG
rs4346144	AGACCTCTTTAAGTAATACTCC	ACT
rs7148078	GGCTTGGGTACGGGAAGC	CGT
rs7148286	CATTAAGCTTGCCAGAAAATCA	ACG
rs3783980	CATCTTCCTCTGCCTCCCA	ACG
rs1549119	CTTCCTCTGCCTCCCATAAAT	CGT
rs1984925	CAGGCACGTGCCACCACA	ACG
rs1477261	AGGAGGAGCCCAAATATGAAA	CGT
rs8016447	CACACCTGGCCATGCTTCC	ACT
rs7494044	CCTGGCCATGCTTCCGTATT	ACG
rs2023288	AATTGTGATTGATTGATTGCGAT	CGT
rs7151685	GTGAGCCACCACATCATCTG	ACT
rs2112135	TCAGGTGATCCTCCTGCCT	ACG
rs2161088	CCAATCACAGCCCACTGCA	ACT
rs4903638	GCCAGAGTGGTCTCCAAC	ACT
rs1477262	AGAGCTCAAGCTGATGTCCT	ACT
rs1477263	TTTTCCTGTTGAGTTCGCATG	ACT
rs1477264	ACCACCTCAGTTTGTCTGTTT	ACG
rs2277917	CCTTGATAACCGCTTGGTCT	ACT
rs2277918	AAAAGCTTCCCGGGGACAG	CGT
rs2277919	AGCTTCCCGGGGACAGCT	ACT
rs1978416	TGAGACTAGCTAATGGAGAGT	ACG
rs3759728	AGCAAATCTACTGCAAACGTG	CGT

dbSNP rs#	Extend Primer	Term Mix
rs6574399	AAGTAGAGCTGCTCCACC	CGT
rs7155336	GAAGACTCGGTCTAAAAAAAAAA	ACT
rs7156186	GCCACTGCACCTGGCCG	ACT
rs7142390	TGGTACTGGCATAAGGATAGA	ACG
rs7145875	CACAAAACCTTAACCTTTTGATTTA	ACT
rs8014635	CAAGAACACTGGTTTTGGTTTT	ACT
rs8015938	CTCAAGTGATCTGCCTGCC	ACT
rs8015313	GATTCTGTACCTGGTTGATCAT	ACT
rs8006315	AACATGGTGAAGCCCCATCT	CGT
rs6574400	GAGATCGCCAGAGACACCA	ACG
rs7140816	TGAGACTCTGTCTCAAATACTA	CGT
rs4566078	CTCAGCTCACTGCAACCTC	ACG
rs7141050	AGCACATAGTAAGTGCCCTAT	ACT
rs3049356	GAATAGTGAAGGTATTGAAATA	ACT
rs4903639	GAGACTCCGTCTCAAAAAAAAAAA	CGT
rs4903641	GGCAACAGAGCGAGACTCC	ACT
rs2364838	CCAGCTACTTGTGAGGCCAA	ACT
rs2364839	AGCCAGACGTGGTGGCAC	ACT
rs4632066	GAGATGGAGGGGGAGCCT	ACT
rs2112136	GGGACTAAGGCTCGCATCC	ACT
rs4641655	GGATTTCTGGGTCCCACTC	ACG
rs4635269	AGCCACCGCGCCCGGCC	ACT
rs4570764	GTGATTATTGGCCGGGCGC	ACT
rs759808	TGCACCACACAGCCTGGG	CGT
rs7150531	AGCAAAGTTAATGGGAGGCC	ACT
rs7154968	AACAAACCTGCATATGTACCC	ACT
rs7146657	CACCCACCACCCCGCCC	ACT
rs7145859	CGGGAGGTGGAGCTTGCA	ACT
rs4903643	GCTCCCTTCTGTCTACTGC	ACT
rs717682	AGGCTGAGGCAGGAGAATC	ACT
rs717683	AAAAGGTGGAGGCCAAAGAC	ACT
rs1477259	CGGAATAATTATATCTGCCTCT	ACT
rs8019064	CAGAGGCAGATATAATTATTCC	ACT
rs8018971	GTCACCTCAGGCTGGAGTGC	CGT
rs1477260	GACGAGGAGGAAAGCCATC	ACT
rs5809851	CACAGCAGTGTCTTTTTTTTTTT	ACT
rs1985149	TTCTTCTCCCTCAGCCTCC	ACG
rs1008988	GGGGATGACCTCTCTGGAG	ACT
rs1008989	GCCAGCTTGGCAGATTGAG	CGT
rs8018222	TGCTGAACGCTGGTCCCC	CGT
rs1006040	TGGAGTGCAGTGGCAAGAC	ACG
rs1006039	CATAGCCAGACCCTATGAGA	ACG
rs1006038	ACTGTGCTCAGTCTATGCTG	ACG
rs8009784	ATGCTTTGCCTTAAAGTGCTG	ACT

dbSNP rs#	Extend Primer	Term Mix
rs4903644	GCCTGGGCAACAGAGCAAG	ACT
rs7149496	GATTCTGTAAGTCTGGTATGAG	ACT
rs6574402	CTGACAAGAAAATGACTGCATA	ACT

Genetic Analysis

[0242] Allelotyping results are shown for cases and controls in Table 23. The allele frequency for the A2 allele is noted in the fifth and sixth columns for osteoarthritis case pools and control pools, respectively, where “AF” is allele frequency. The allele frequency for the A1 allele can be easily calculated by subtracting the A2 allele frequency from 1 (A1 AF = 1-A2 AF). For example, the SNP rs7143926 has the following case and control allele frequencies: case A1 (A) = 0.75; case A2 (T) = 0.25; control A1 (A) = 0.71; and control A2 (T) = 0.29, where the nucleotide is provided in paranthesis. Some SNPs are labeled “untyped” because of failed assays.

TABLE 23

dbSNP rs#	Position in SEQ ID NO: 3	Chromosome Position	A1/A2 Allele	F A2 Case AF	F A2 Control AF	F p- Value
rs7143926	218	76161268	A/T	0.25	0.29	0.216
rs1549071	1440	76162490	C/T	0.15	0.20	0.098
rs8012858	1442	76162492	C/T	0.93	0.95	0.335
rs7155611	2611	76163661	C/T	0.02	0.02	0.949
rs176941	4317	76165367	A/C	0.31	0.35	0.271
rs176942	4724	76165774	A/G	0.02	0.02	0.911
rs176943	4788	76165838	G/T	0.13	0.18	0.037
rs176944	5202	76166252	G/T	0.09	0.14	0.107
rs4365221	5780	76166830	C/T			
rs3168952	5974	76167024	C/T			
rs176945	6644	76167694	C/G	0.95	0.96	0.801
rs176946	7430	76168480	A/G	0.10	0.15	0.054
rs176947	7938	76168988	C/T	0.10	0.08	0.473
rs176948	8095	76169145	C/T	0.31	0.35	0.132
rs176949	8183	76169233	A/C	0.03	0.02	0.887
rs176950	8312	76169362	C/T	0.78	0.70	0.008
rs176951	8352	76169402	A/C			
rs7156905	9348	76170398	C/T	0.89	0.90	0.794
rs3217197	9378	76170428	-/TCTC	0.29	0.35	0.036
rs2270443	9617	76170667	A/G	0.39	0.34	0.176
rs176952	9727	76170777	C/T	0.17	0.24	0.018
rs176953	9834	76170884	C/T			
rs176954	9899	76170949	G/T	0.43	0.52	0.010
rs176955	10211	76171261	C/T	0.12	0.18	0.028
rs3214416	10377	76171427	-/T	0.91	0.89	0.544
rs176956	10695	76171745	C/T	0.51	0.49	0.492
rs2544566	10729	76171779	C/G			
rs2544567	10730	76171780	C/T			
rs176957	11433	76172483	A/G			
rs176958	11951	76173001	C/G	0.02	NA	NA

dbSNP rs#	Position in SEQ ID NO: 3	Chromosome Position	A1/A2 Allele	F A2 Case AF	F A2 Control AF	F p- Value
rs176959	12697	76173747	C/T	0.30	0.34	0.147
rs1802227	12982	76174032	A/C	0.92	0.95	0.332
rs176961	14419	76175469	C/T	0.51	0.47	0.158
rs176962	14501	76175551	C/T	0.82	0.79	0.192
rs7401285	14983	76176033	A/C			
rs176963	15280	76176330	C/T	0.51	0.46	0.155
rs176964	15475	76176525	A/G	0.53	0.49	0.197
rs4903631	15888	76176938	A/G			
rs4903632	15976	76177026	A/T			
rs176965	16307	76177357	A/C	0.55	0.52	0.368
rs4903633	16442	76177492	A/C	0.83	0.83	0.970
rs176966	17255	76178305	C/T			
rs176968	18948	76179998	G/T	0.23	0.27	0.246
rs176969	19435	76180485	A/T	0.14	0.20	0.052
rs176970	19753	76180803	C/T	0.35	0.38	0.328
rs7149198	20021	76181071	C/T			
rs7147918	20022	76181072	A/C			
rs7148685	20503	76181553	A/G	0.19	0.18	0.669
rs1184232	20590	76181640	G/T	0.16	0.19	0.316
rs1184233	21804	76182854	G/T	0.36	0.36	0.895
rs1184234	21919	76182969	C/T	0.36	0.35	0.797
rs7401998	21990	76183040	A/T			
rs176974	22412	76183462	A/G			
rs6574390	22536	76183586	C/T			
rs176975	23432	76184482	A/G	0.18	0.23	0.147
rs176976	23468	76184518	G/T	0.86	0.80	0.087
rs176977	23772	76184822	C/T	0.42	0.41	0.794
rs8013727	24325	76185375	C/T			
rs176978	24773	76185823	C/T	0.10	0.12	0.512
rs2111829	26274	76187324	C/T	0.02	NA	
rs176980	27440	76188490	C/G	0.79	0.73	0.018
rs5809848	28561	76189611	-/ACAG	0.11	0.16	0.091
rs5809849	30071	76191121	-/A	0.60	0.57	0.355
rs4383070	31764	76192814	A/T			
rs7493652	33008	76194058	C/T			
rs2112133	35310	76196360	A/T			
rs1963833	35460	76196510	A/C			
rs6574391	37112	76198162	A/G	0.69	0.63	0.064
rs7155062	37285	76198335	A/G	0.17	0.18	0.878
rs4899674	37747	76198797	C/T	0.57	0.52	0.201
rs8022516	38057	76199107	C/T	0.57	0.51	0.135
rs7140838	38859	76199909	A/C	0.17	0.17	0.957
rs7141127	38860	76199910	A/G			
rs6574392	39525	76200575	A/G	0.27	0.32	0.099
rs8003691	40216	76201266	A/G	0.70	0.63	0.029
rs8003979	40281	76201331	C/T	0.10	0.15	0.024
rs8010541	41453	76202503	C/G	0.38	0.38	0.993
rs8016416	42091	76203141	A/T	0.09	0.14	0.035
rs8016175	42513	76203563	A/G			
rs7154571	42935	76203985	C/T			
rs7158826	42985	76204035	A/G			
rs7159310	43003	76204053	A/G	0.62	NA	
rs7401900	43281	76204331	A/G			
rs7160355	43716	76204766	C/T			
rs2032781	43866	76204916	A/G	0.80	0.74	0.047
rs6574394	44234	76205284	G/T	0.61	0.54	0.091
rs8007598	44596	76205646	A/G	0.09	0.10	0.734

dbSNP rs#	Position in SEQ ID NO: 3	Chromosome Position	A1/A2 Allele	F A2 Case AF	F A2 Control AF	F p- Value
rs2267767	44871	76205921	C/T			
rs6574395	45005	76206055	A/G	0.10	0.14	0.203
rs7150066	45282	76206332	A/C	0.91	NA	
rs7492334	47178	76208228	A/C			
rs4359361	47816	76208866	G/T			
rs4605089	47887	76208937	A/G			
rs7146446	48134	76209184	C/T	0.09	0.09	0.981
rs4346144	48135	76209185	A/G	0.83	0.85	0.368
rs7148078	48276	76209326	G/T	0.44	0.50	0.098
rs7148286	48400	76209450	C/T	0.96	0.96	0.893
rs3783980	48798	76209848	A/G	0.15	0.20	0.073
rs1549119	48803	76209853	A/T	0.18	0.25	0.027
rs1984925	49146	76210196	C/T	0.04	0.04	0.882
rs1477261	49969	76211019	A/T			
rs8016447	51059	76212109	A/G	0.10	0.15	0.049
rs7494044	51064	76212114	C/T			
rs2023288	53285	76214335	A/T	0.97	0.98	0.774
rs7151685	54560	76215610	C/T			
rs2112135	54748	76215798	A/G	0.05	NA	
rs2161088	54785	76215835	C/G			
rs4903638	55102	76216152	C/G	0.59	0.59	0.975
rs1477262	55644	76216694	A/G	0.12	0.17	0.040
rs1477263	55705	76216755	G/T	0.18	0.23	0.057
rs1477264	55841	76216891	A/G	0.45	0.42	0.271
rs2277917	56623	76217673	C/G	0.30	0.36	0.039
rs2277918	56825	76217875	A/C	0.49	0.45	0.232
rs2277919	56827	76217877	A/G	0.20	0.17	0.310
rs1978416	56892	76217942	C/T	0.79	0.73	0.074
rs3759728	59150	76220200	A/T	0.13	0.18	0.083
rs6574399	59958	76221008	A/T	0.33	0.36	0.396
rs7155336	60231	76221281	C/T	0.25	0.28	0.250
rs7156186	60524	76221574	A/G	0.85	0.85	0.965
rs7142390	61871	76222921	C/T			
rs7145875	62226	76223276	C/T			
rs8014635	63230	76224280	G/T	0.07	0.11	0.062
rs8015938	63468	76224518	G/T	0.08	0.07	0.693
rs8015313	63787	76224837	C/T	0.67	0.71	0.135
rs8006315	65732	76226782	A/C			
rs6574400	65989	76227039	A/G	0.75	0.70	0.099
rs7140816	68832	76229882	G/T	0.54	0.48	0.095
rs4566078	69904	76230954	C/T			
rs7141050	70365	76231415	A/G			
rs3049356	70886	76231936	-T/ATC	0.64	0.69	0.091
rs4903639	73088	76234138	A/T			
rs4903641	73103	76234153	C/T	0.54	0.66	~0.0001
rs2364838	75934	76236984	C/T			
rs2364839	75966	76237016	C/T	0.18	0.18	0.988
rs4632066	76273	76237323	C/T	0.66	0.66	0.961
rs2112136	77943	76238993	C/T	0.70	0.64	0.064
rs4641655	78466	76239516	C/T	0.52	0.48	0.174
rs4635269	78861	76239911	C/T			
rs4570764	78872	76239922	A/G	0.55	0.68	~0.0001
rs759808	79836	76240886	G/T	0.12	0.18	0.043
rs7150531	80908	76241958	C/T	0.33	0.31	0.491
rs7154968	81509	76242559	C/G	0.03	NA	
rs7146657	83576	76244626	C/T	0.57	NA	NA
rs7145859	83662	76244712	C/G			

dbSNP rs#	Position in SEQ ID NO: 3	Chromosome Position	A1/A2 Allele	F A2 Case AF	F A2 Control AF	F p- Value
rs4903643	83782	76244832	C/T	0.10	0.14	0.074
rs717682	84282	76245332	G/T	0.11	0.13	0.624
rs717683	84444	76245494	A/G	0.79	0.75	0.121
rs1477259	85129	76246179	C/G	0.11	0.16	0.022
rs8019064	85151	76246201	A/G	0.90	0.93	0.192
rs8018971	85296	76246346	A/C			
rs1477260	85809	76246859	C/G	0.12	0.16	0.085
rs5809851	86387	76247437	-/T	0.30	0.30	0.993
rs1985149	86494	76247544	A/G	0.22	0.23	0.892
rs1008988	89786	76250836	A/G	0.61	0.58	0.380
rs1008989	89894	76250944	A/T	0.14	0.18	0.172
rs8018222	90122	76251172	G/T			
rs1006040	92067	76253117	A/G	0.13	0.18	0.092
rs1006039	92187	76253237	C/T	0.06	0.10	0.133
rs1006038	92312	76253362	A/G	0.19	0.24	0.114
rs8009784	92824	76253874	G/T	0.13	0.18	0.037
rs4903644	93733	76254783	C/T	0.41	0.38	0.383
rs7149496	96553	76257603	C/G			
rs6574402	96941	76257991	A/C	0.12	0.17	0.037

[0243] Allelotyping results were considered particularly significant with a calculated p-value of less than or equal to 0.05 for allelotype results. These values are indicated in bold. The allelotyping p-values were plotted in Figure 1C for the discovery cohort. The position of each SNP on the chromosome is presented on the x-axis. The y-axis gives the negative logarithm (base 10) of the p-value comparing the estimated allele in the case group to that of the control group. The minor allele frequency of the control group for each SNP designated by an X or other symbol on the graphs in Figure 1C can be determined by consulting Table 23. For example, the left-most X on the left graph is at position 76161268. By proceeding down the Table from top to bottom and across the graphs from left to right the allele frequency associated with each symbol shown can be determined.

[0244] To aid the interpretation, multiple lines have been added to the graph. The broken horizontal lines are drawn at two common significance levels, 0.05 and 0.01. The vertical broken lines are drawn every 20kb to assist in the interpretation of distances between SNPs. Two other lines are drawn to expose linear trends in the association of SNPs to the disease. The light gray line (or generally bottom-most curve) is a nonlinear smoother through the data points on the graph using a local polynomial regression method (W.S. Cleveland, E. Grosse and W.M. Shyu (1992) Local regression models. Chapter 8 of Statistical Models in S eds J.M. Chambers and T.J. Hastie, Wadsworth & Brooks/Cole.). The black line provides a local test for excess statistical significance to identify regions of association. This was created by use of a 10kb sliding window with 1kb step sizes. Within each window, a chi-square goodness of fit test was applied to compare the proportion of SNPs that were significant at a test wise

level of 0.01, to the proportion that would be expected by chance alone (0.05 for the methods used here). Resulting p-values that were less than 10^{-8} were truncated at that value.

[0245] Finally, the exons and introns of the genes in the covered region are plotted below each graph at the appropriate chromosomal positions. The gene boundary is indicated by the broken horizontal line. The exon positions are shown as thick, unbroken bars. An arrow is placed at the 3' end of each gene to show the direction of transcription.

Example 7

In Vitro Production of Target Polypeptides

[0246] cDNA is cloned into a pIVEX 2.3-MCS vector (Roche Biochem) using a directional cloning method. A cDNA insert is prepared using PCR with forward and reverse primers having 5' restriction site tags (in frame) and 5-6 additional nucleotides in addition to 3' gene-specific portions, the latter of which is typically about twenty to about twenty-five base pairs in length. A Sal I restriction site is introduced by the forward primer and a Sma I restriction site is introduced by the reverse primer. The ends of PCR products are cut with the corresponding restriction enzymes (*i.e.*, Sal I and Sma I) and the products are gel-purified. The pIVEX 2.3-MCS vector is linearized using the same restriction enzymes, and the fragment with the correct sized fragment is isolated by gel-purification. Purified PCR product is ligated into the linearized pIVEX 2.3-MCS vector and *E. coli* cells transformed for plasmid amplification. The newly constructed expression vector is verified by restriction mapping and used for protein production.

[0247] *E. coli* lysate is reconstituted with 0.25 ml of Reconstitution Buffer, the Reaction Mix is reconstituted with 0.8 ml of Reconstitution Buffer; the Feeding Mix is reconstituted with 10.5 ml of Reconstitution Buffer; and the Energy Mix is reconstituted with 0.6 ml of Reconstitution Buffer. 0.5 ml of the Energy Mix was added to the Feeding Mix to obtain the Feeding Solution. 0.75 ml of Reaction Mix, 50 μ l of Energy Mix, and 10 μ g of the template DNA is added to the *E. coli* lysate.

[0248] Using the reaction device (Roche Biochem), 1 ml of the Reaction Solution is loaded into the reaction compartment. The reaction device is turned upside-down and 10 ml of the Feeding Solution is loaded into the feeding compartment. All lids are closed and the reaction device is loaded into the RTS500 instrument. The instrument is run at 30°C for 24 hours with a stir bar speed of 150 rpm. The pIVEX 2.3 MCS vector includes a nucleotide sequence that encodes six consecutive histidine amino acids on the C-terminal end of the target polypeptide for the purpose of protein purification. Target polypeptide is purified by contacting the contents of reaction device with resin modified with Ni^{2+} ions. Target polypeptide is eluted from the resin with a solution containing free Ni^{2+} ions.

Example 8

Cellular Production of Target Polypeptides

[0249] Nucleic acids are cloned into DNA plasmids having phage recombination sites and target polypeptides are expressed therefrom in a variety of host cells. Alpha phage genomic DNA contains short sequences known as attP sites, and *E. coli* genomic DNA contains unique, short sequences known as attB sites. These regions share homology, allowing for integration of phage DNA into *E. coli* via directional, site-specific recombination using the phage protein Int and the *E. coli* protein IHF. Integration produces two new att sites, L and R, which flank the inserted prophage DNA. Phage excision from *E. coli* genomic DNA can also be accomplished using these two proteins with the addition of a second phage protein, Xis. DNA vectors have been produced where the integration/excision process is modified to allow for the directional integration or excision of a target DNA fragment into a backbone vector in a rapid *in vitro* reaction (Gateway™ Technology (Invitrogen, Inc.)).

[0250] A first step is to transfer the nucleic acid insert into a shuttle vector that contains attL sites surrounding the negative selection gene, ccdB (*e.g.* pENTER vector, Invitrogen, Inc.). This transfer process is accomplished by digesting the nucleic acid from a DNA vector used for sequencing, and to ligate it into the multicloning site of the shuttle vector, which will place it between the two attL sites while removing the negative selection gene ccdB. A second method is to amplify the nucleic acid by the polymerase chain reaction (PCR) with primers containing attB sites. The amplified fragment then is integrated into the shuttle vector using Int and IHF. A third method is to utilize a topoisomerase-mediated process, in which the nucleic acid is amplified via PCR using gene-specific primers with the 5' upstream primer containing an additional CACC sequence (*e.g.*, TOPO® expression kit (Invitrogen, Inc.)). In conjunction with Topoisomerase I, the PCR amplified fragment can be cloned into the shuttle vector via the attL sites in the correct orientation.

[0251] Once the nucleic acid is transferred into the shuttle vector, it can be cloned into an expression vector having attR sites. Several vectors containing attR sites for expression of target polypeptide as a native polypeptide, N-fusion polypeptide, and C-fusion polypeptides are commercially available (*e.g.*, pDEST (Invitrogen, Inc.)), and any vector can be converted into an expression vector for receiving a nucleic acid from the shuttle vector by introducing an insert having an attR site flanked by an antibiotic resistant gene for selection using the standard methods described above. Transfer of the nucleic acid from the shuttle vector is accomplished by directional recombination using Int, IHF, and Xis (LR clonase). Then the desired sequence can be transferred to an expression vector by carrying out a one hour incubation at room temperature with Int, IHF, and Xis, a ten minute incubation at 37°C with proteinase K, transforming bacteria and allowing expression for one hour, and then plating on selective media. Generally, 90% cloning efficiency is achieved by this method. Examples of expression vectors

are pDEST 14 bacterial expression vector with att7 promoter, pDEST 15 bacterial expression vector with a T7 promoter and a N-terminal GST tag, pDEST 17 bacterial vector with a T7 promoter and a N-terminal polyhistidine affinity tag, and pDEST 12.2 mammalian expression vector with a CMV promoter and neo resistance gene. These expression vectors or others like them are transformed or transfected into cells for expression of the target polypeptide or polypeptide variants. These expression vectors are often transfected, for example, into murine-transformed adipocyte cell line 3T3-L1, (ATCC), human embryonic kidney cell line 293, and rat cardiomyocyte cell line H9C2.

[0252] Modifications may be made to the foregoing without departing from the basic aspects of the invention. Although the invention has been described in substantial detail with reference to one or more specific embodiments, those of skill in the art will recognize that changes may be made to the embodiments specifically disclosed in this application, yet these modifications and improvements are within the scope and spirit of the invention, as set forth in the claims which follow. All publications or patent documents cited in this specification are incorporated herein by reference as if each such publication or document was specifically and individually indicated to be incorporated herein by reference.

[0253] Citation of the above publications or documents is not intended as an admission that any of the foregoing is pertinent prior art, nor does it constitute any admission as to the contents or date of these publications or documents. U.S. patents and other publications referenced herein are hereby incorporated by reference.

Nucleotide and Amino Acid Sequence Examples

[0254] Table A includes information pertaining to the incident polymorphic variant associated with osteoarthritis identified herein. Public information pertaining to the polymorphism and the genomic sequence that includes the polymorphism are indicated. The genomic sequences identified in Table A may be accessed at the http address www.ncbi.nih.gov/entrez/query.fcgi, for example, by using the publicly available SNP reference number (*e.g.*, rs552). The chromosome position refers to the position of the SNP within NCBI's Genome Build 34, which may be accessed at the following http address: www.ncbi.nlm.nih.gov/mapview/map_search.cgi?chr=hum_chr.inf&query=. The "Contig Position" provided in Table A corresponds to a nucleotide position set forth in the contig sequence (see "Contig Accession No."), and designates the polymorphic site corresponding to the SNP reference number. The sequence containing the polymorphisms also may be referenced by the "Nucleotide Accession No." set forth in Table A. The "Sequence Identification" corresponds to cDNA sequence that encodes associated target polypeptides (*e.g.*, Q96FX2). The position of the SNP within the cDNA sequence is provided in the "Sequence Position" column of Table A. If the SNP falls within an exon, the corresponding amino acid position (and amino acid change, if applicable) is provided as well. Also, the allelic variation at the

polymorphic site and the allelic variant identified as associated with osteoarthritis is specified in Table A. All nucleotide and polypeptide sequences referenced and accessed by the parameters set forth in Table A are incorporated herein by reference. Genomic nucleotide sequences for *KIAA0296*, *chrom 4* and *SNW1* regions are set forth in SEQ ID NO: 1-3, respectively. A polymorphism in Table A designated by "AA" is present in the genomic nucleotide sequence of SEQ ID NO: 4, which follows Table A.

Table A

RS_ID	Chromosome	Chrom Position	Contig Accession No. [1]	Contig Position	Nucleotide Accession No. [2]	Sequence Position	Amino Acid Position	Locus	Locus ID	A [3]	Allelic Variability	OA Assoc. Allele
552	3	16276963	Hs3_22673_34:16	16241963	XM_209584	intergenic		Q96FX2	253631; 92106	R	[A/G]	A
12904	1	152323489	Hs1_79549_34:1	1556529	NM_004428 NM_018845	mma-utr locus-region		EFNA1 LOC55974	1942 55974	F	[A/G]	A
2282146	20	49881706	Hs20_11519_34:8	14249192	NM_002827	coding-synon	303	PTPN1	5770	R	[C/T]	T
734784	20	44409056	Hs20_11519_34:8	8776542	NM_002251	coding-nonsynon	V489I	KCNS1	3787	R	[G/A]	G
1042164	19	13125398	Hs19_11452_34:1	4527200	NM_004907	coding-nonsynon	V133A	ETR101	9592	R	[T/C]	T
749670	16	31124685	Hs16_24968_34:1	2488292	NM_014699	coding-nonsynon	G327E	KIAA0296	9726	F	[C/T]	T
955592	2	85570358	Hs2_22340_34:13	64411756	NM_032213	coding-nonsynon	I70T	FLJ21977	84173	R	[T/C]	C
1143016	1	2209625	Hs1_4507_34:16	317874	NM_002617	coding-synon	93	PEX10	5192	R	[T/C]	T
755248	1	39408404	Hs1_33153_34:6	1601557	NM_024732	mma-utr		FLJ14351	79787	R	[G/A]	G
1055055	1	42293810	Hs1_33153_34:6	4486963	NM_173642	coding-synon	308	MGC47816	284716	F	[A/G]	A
835409	1	59157267	Hs1_33153_34:6	21350420	NM_018291	mma-utr		FLJ10986	55277	F	[T/G]	G
927663	1	155318902	Hs1_79549_34:1	4551942	AL138899	10739		LOC254079	254079	F	[T/G]	G
8162	2	42552684	Hs2_22340_34:13	21394082	NM_004718	mma-utr		COX7A2L	9167	F	[A/G]	G
831038	2	170404402	Hs2_5560_34:14	20411275	NM_004525	intron		LRP2	4036	F	[C/T]	T
33079	2	231577157	Hs2_5560_34:14	81584030	NM_003113	intron		SP100	6672	R	[G/A]	A
1710880	3	11027339	Hs3_22673_34:16	10992339	AC024910.5	71095		SLC6A1	6529	F	[C/A]	A
4472029	3	102614466	Hs3_5769_34:14	7788711	NM_020357	intron		PCNP	57092	F	[T/A]	A
799570	3	113007639	Hs3_5769_34:14	18181884	NM_145753	intron		LL5beta	90102	F	[A/G]	G
1282730	3	113026933	Hs3_5769_34:14	18201178	NM_018394	intron		FLJ11342	55347	R	[G/A]	A
1518875	3	188430421	Hs3_5769_34:14	93804666	none	intergenic		none	none	R	[T/C]	C
1568694	4	8584835	Hs4_6464_34:15	505708	NM_003501	intron		ACOX3	8310	R	[G/A]	A

RS_ID	Chromosome	Chrom Position	Contig Accession No. [1]	Contig Position	Nucleotide Accession No. [2]	Sequence Position	Amino Acid Position	Locus	Locus ID	A [3]	Allelic Variability	OA Assoc. Allele
905042	4	16229175	Hs4_6473_34:15	7153650	none	intergenic		none	none	R	[A/T]	A
1957723	4	36919171	Hs4_16453_34:15	4170634	none	intergenic		none	none	R	[G/A]	A
794018	4	40066604	Hs4_16453_34:15	7318067	none	intergenic		none	none	R	[G/A]	G
707723	4	47757791	Hs4_6395_34:10	7544215	NM_006587	UTR/intergenic		PRSC	10699	F	[C/T]	T
893861	4	47872633	Hs4_6395_34:10	7659057	NM_000087	mma-utr		CNGA1	1259	R	[G/A]	G
1914903	4	125442695	Hs4_16510_34:16	49479005	none	locus-region		LOC377201	377201	R	[G/A]	A
2062232	4	163485648	Hs4_16762_34:16	24456077	NM_020116	intron		DKFZp566D234	56884	F	[C/T]	T
26609	5	53447781	Hs5_6588_34:13	3996639	NM_019087	intron		FLJ20051	54622	R	[A/T]	T
1370987	5	79365937	Hs5_6870_34:13	8673996	XM_293971	locus-region		LOC345778	345778	F	[A/G]	A
1012414	5	150535958	Hs5_29448_34:10	11670384	NM_001155	intron		ANXA6	309	R	[G/A]	G
435903	5	156713884	Hs5_23289_34:11	1542547	NM_014376	intron		CYFIP2	26999	R	[G/A]	G
1248	5	156742512	Hs5_23289_34:11	1571175	NM_014376	intron		CYFIP2	26999	F	[T/A]	T
703508	5	169797195	Hs5_23289_34:11	14625858	NM_004137	mma-utr		KCNMB1	3779	R	[G/A]	A
226465	6	1755892	Hs6_35042_34:3	1750892	NM_001500	intron		GMDS	2762	R	[G/C]	C
241448	06	32785099	NT_033951	4177541	NM_000544	UTR		TAP2	6891	F	[C/T]	C
763155	6	35240628	Hs6_7749_34:13	25990900	NM_152753	intron		CEGF3	222663	R	[A/C]	A
1040461	6	57102190	Hs6_7749_34:13	47852462	NM_016277	coding-nonsynon	S207G	RAB23	51715	R	[T/C]	C
462832	6	111731861	Hs6_25897_34:13	15855720	NM_002912	intron		REV3L	5980	R	[A/T]	A
804194	6	112053555	Hs6_25897_34:13	16177414	NM_002037	intron		FYN	2534	R	[T/C]	C
1022646	6	112074901	Hs6_25897_34:13	16198760	NM_002037	intron		FYN	2534	F	[A/G]	A
1569112	7	699341	Hs7_7976_34:14	250677	NM_006869	intron		CENTA1	11033	R	[G/A]	G
805623	10	29478204	Hs10_8862_34:15	11449523	none	intergenic		none	none	F	[A/G]	G
1019850	11	83985464	Hs11_34082_34:6	14458185	NM_001364	intron		DLG2	1740	R	[A/T]	A
1599931	12	56545117	Hs12_29578_34:1	20402156	none	intergenic		none	none	F	[A/G]	G
AA	13	29711866			NM_006644	exonic		HSP105B	10808	F	[A/G]	G
279941	13	101396169	Hs13_10109_34:1	16787844	NM_000452	mma-utr		SLC10A2	6555	F	[T/G]	G

RS_ID	Chromosome	Chrom Position	Contig Accession No. [1]	Contig Position	Nucleotide Accession No. [2]	Sequence Position	Amino Acid Position	Locus	Locus ID	A [3]	Allelic Variability	OA Assoc. Allele
1062230	14	23479277	Hs14_26604_34:1	5409277	NM_014178	mma-utr		STXBP6	29091	F	[C/T]	C
1859911	14	70531426	Hs14_26604_34:1	52461426	NM_004296	intron		RGS6	9628	R	[T/C]	T
1477261	14	76211019	Hs14_26604_34:1	58141019	NM_012245	intron		SNW1	22938	F	[T/A]	T
1191119	14	98332328	Hs14_26604_34:1	80262328	NM_004434	intron		EML1	2009	R	[G/A]	G
657780	15	60862497	Hs15_10351_34:1	33936998	none	intergenic		none	none	F	[A/G]	A
1393890	15	95036282	Hs15_10431_34:1	12272041	XM_096908	UTR		LOC145945	145945	R	[G/C]	C
1478714	16	7132995	Hs16_10709_34:1	4474136	NM_018723	intron		A2BP1	54715	R	[G/A]	G
868213	16	66996694	Hs16_10655_34:1	15942010	NM_178516	intron		LOC283849	283849	F	[C/T]	C
690115	17	73471192	Hs17_10798_34:1	6766230	NM_178128	mma-utr		LOC283985	283985	R	[G/A]	G
1465501	18	18066783	Hs18_11123_34:1	1303898	none	intergenic		none	none	F	[A/G]	G
899173	19	14094734	Hs19_11452_34:1	5496536	NM_018154	intron		ASF1B	55723	F	[C/T]	C
10477	20	38236897	Hs20_11519_34:8	2604383	NM_015568	mma-utr		PPP1R16B	26051	F	[C/T]	T
926393	20	38331457	Hs20_11519_34:8	2698943	NM_021931	intron		DHX35	60625	F	[C/T]	C
465271	21	26507612	Hs21_11669_34:9	13247612	none	intergenic		none	none	F	[C/T]	C
13847	21	44259022	Hs21_11672_34:1	715558	NM_020132	locus-region		AGPAT3	56894	F	[A/G]	G
738658	22	30168847	Hs22_11677_34:9	11234862	NM_019843	intron		EIF4ENIF1	56478	F	[C/A]	C

[1] Contig Accession Number which can be found in the NCBI Database:
http address: www.ncbi.nih.gov/entrez/query.fcgi

[2] Sequence Identification or Nucleotide Accession Number which can be found in the NCBI Database:
http address: www.ncbi.nih.gov/entrez/query.fcgi

[3] "A" column is the sequence orientation ("F" is forward, "R" is reverse).

AA genomic sequence (SEQ ID NO: 4)

TCATTAGCTTTTTTCAGTTTTTTCACATTCCTGATACAGACGTAGGAGTGCTCGTATTTT
GGATTTTGCATCCAACTTGTACTTAGTTTTAAATTCTGCACA[A/G]AAATGTTCCACT
AACTTTTCATCGAAGTTTTTTCCTCCTAAGAAAGGATCAAAAGCTGTTCCCAGTACC
TAATTTGGTTGAAACAACAAATAGTCTGGTT

[0255] Following are genomic nucleotide sequences for a *KIAA0296* region (SEQ ID NO: 1), a *chrom 4* region (SEQ ID NO: 2), and a *SNW1* region (SEQ ID NO: 3). The following nucleotide representations are used throughout: "A" or "a" is adenosine, adenine, or adenylic acid; "C" or "c" is cytidine, cytosine, or cytidylic acid; "G" or "g" is guanosine, guanine, or guanylic acid; "T" or "t" is thymidine, thymine, or thymidylic acid; and "I" or "i" is inosine, hypoxanthine, or inosinic acid. Exons are indicated in italicized lower case type, introns are depicted in normal text lower case type, and polymorphic sites are depicted in bold upper case type. SNPs are designated by the following convention: "R" represents A or G, "M" represents A or C; "W" represents A or T; "Y" represents C or T; "S" represents C or G; "K" represents G or T; "V" represents A, C or G; "H" represents A, C, or T; "D" represents A, G, or T; "B" represents C, G, or T; and "N" represents A, G, C, or T.

KIAA0296 genomic sequence (SEQ ID NO: 1)

>16:31076951-31174000

1	ccccaccccc	caacagctgc	acagtctgga	gcgaatatac	acgcccacca	cccacacacc
61	caagacccaa	tacacttttt	taaactttat	ttttacttct	atztatttat	ttttaattat
121	tttttaaaaa	tctaattaga	gatgaggtct	taggctgggc	acagtggctc	atgcctgtaa
181	ccccagcact	tcgggaggcc	gaggcaggca	gatacagagg	cgggaggatc	acgaggtcag
241	gagttcRaga	ccagcctggc	caatatgggtg	aaaccccatc	tctgctaaaa	atacaaaaat
301	gagctgggcg	cgggtggtgtg	cacctgtaat	ctcagctact	tgggaggctg	aggcagaatt
361	gtttgaactc	aggaggcgga	tgctgcagtg	agctgagatc	gtgccactgc	actccagtct
421	gggagacaga	gcgagactac	gtctcaaaa	aaacaaaca	acaaacaaca	acaacaaaaa
481	cagagataag	gtcttggcat	gttgcccagg	ctggtctcaa	gtcctgggct	caaaggattc
541	tectgcctca	gcctcccaaa	gtgctaggat	tacaggcgtg	aaccactgca	cccaccctac
601	tttttttttt	tttttttttt	atacaggatc	tcactctgtc	acccgggctg	gagtgcagtg
661	gcaagatcac	tgctgactgt	acccttgacc	tcagggaactc	aagtgatcct	cctgcctcag
721	cctcctgagt	agctgggact	acaggagagc	gccagcacac	ctgggtaatt	aagatttttt
781	ttgtagagac	agacgctatg	ttgcccaggc	tgctctcgaa	ctcctggcct	caagtatac
841	acccttggcc	tcctaaagtg	ctgggatcac	aggcatgagc	cactgcacct	agcctaatat
901	agttaatatc	cccgtaagg	ctgctcagag	ggcctgagag	gaacaaagg	ctcagctctg
961	gagagctcca	ccccagcgc	caatctctct	aaatggcctc	tttcctctcc	atattccacc
1021	acaaggcttg	gagtccagct	tcctgtgacc	ttaagtcacc	attccaaagc	cctgcgatct
1081	caccagaga	ccacaagtga	aataatatta	taatcctgag	aagtttagtg	gaccaagatg
1141	gcatgccatc	aagacgctga	gaaacaaaga	ggaagatggg	accagggggc	ccagaagacg
1201	ctggaaccca	cagtattaaa	agctcagaga	ggctgggcac	agtggctcac	acctgtaatc
1261	ccagcacttt	gggaggccaa	ggtgggtgga	tcacttgagc	ccaggggttt	gagaacagcc
1321	tgggcaacat	ggcgaaaccc	agtctctacc	aaaaaatata	caaaaattag	ccaggcatgg
1381	tggtgcgtgc	cttagtacca	gctacttggg	aggctgaggc	aggaggattg	actgaacctg
1441	agagcacacc	actgcactcc	agcctggatg	acagaaccag	acctgacctc	aaagagaaga
1501	aaaaaaaaaa	aaaaaaaaag	cccagagggg	agggYaccct	caacagtttt	ccagcccctt
1561	ccacatcctt	cctaacctca	cttgatagtg	ttcaagtcct	accttaggca	aggcagaaat
1621	tataggacca	agccgcctaa	tggggaaatt	gagtcaccaga	gagaagtaat	gcattattta
1681	agatcccatg	caggactatg	agtccaggggt	ccaagagccc	ttccaccgtg	tgccactcag

1741	agacacagag	taggaggggg	aaggggggtcg	ggtggcaggg	gacaaaagat	gcaggaggca
1801	agcagcagtg	actgaagagg	cagagggtga	catgaaagac	ccaggagcag	agaatctttc
1861	cttatcatct	ccaggggaca	ccactgggca	gggcttggcc	tccggaaaaa	ccctgcattc
1921	cctctgtggg	ttcatcaggg	caccactctc	ctactagctg	ggtttttttt	ttttgttttg
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2041	cagctcactg	taacctccac	ctcccattgt	caagcaatcc	tcctgtctca	gcctcccaag
2101	tagctgggat	tacaggcacc	tgccatcatg	cctggctaata	ttttgtatgt	ttgtagagac
2161	agggtttctg	catgttggcc	aggctgggtc	ccaactcctg	gcctcaggtg	atctgcctgc
2221	ctcagcctcc	caaagtgtct	ggattacagg	catgagccac	cacaccctgc	ctgagctggg
2281	ttttaacagg	aagaggagaa	gagccaaaac	tcctcacata	gaatcacaca	gcacttgaca
2341	gtttccaacc	tcacatcac	tgaagttag	agcagccgat	acccaYaaag	atgatctccc
2401	catcccccta	cagttaccca	ctgtgcagag	ggagatccac	acttagagac	aggaagcgat
2461	ttccagaagt	ccatagcaac	tcagtccag	gaatctaggt	ttcctgacca	gggcatagca
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2761	aatgactgaa	tgttgctgtg	catggtgggt	catgcctgta	atcccagcac	tttggaagc
2821	tgaggcagaa	ggattgctta	agcccaggag	ttagagacca	gcttggacaa	catagtga
2881	ccgcatctcg	taaaaatttt	taaaaataaa	aaatgagtga	atatctagat	agccaggatt
2941	agagaagtgt	acagtcaga	aagcctgaag	cctaaagaag	accaaggaa	caggggcttt
3001	atcctcagat	acatgaaagc	ctgaaattct	gtccacaagt	atttatagag	ggcccgtaat
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3181	aacacttttc	ttagcctgag	ctgccctgac	atggtctgac	ggctcacaa	gtgggtagtg
3241	cagccgggct	gcagtgttca	aggagggcgc	cggctggcgc	cccacctgtc	agagctgcg
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3361	tccttgccca	cacaaccctg	caattttctg	acgctgacga	ctcgatcct	attatttccc
3421	gattttcaag	gtcccattgat	gctgacagcc	ccaaatgcta	agtcgtcagt	ccgcccacgc
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3781	tacgtacaaa	tgacgtattc	ctaccccttt	tggcaaccag	atttccgttg	gaagatgcaa
3841	cggttccggt	cacggtagca	agttctcgcg	tccaggcata	tcgcgttccg	ctcggggcgc
3901	aacaacttcc	gactccacct	tcccagcctc	gggcaaggaa	gagacgcgac	catgtgcgca
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4261	agacaggtga	gacgccaggg	cagcggggat	ggggacgggc	ggacgaactg	gaacgcagga
4321	cttctggtct	tcgggatagg	gaggggtggc	tgatggccag	gaaggaaagt	cccggaaagc
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4621	catatctctt	tcagccctct	cggtcaccct	ccccagggtc	ggacaattcg	gcagactatt
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5401	ccatagagcc	ccagaaggag	gaagctgatg	agaactataa	ctccgtcaac	acaagaatga
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5521	agtattagat	gacaggtgta	tgaagggaag	gcctgcagag	atcatggagt	ccaattggat

5581	gactttttcca	aatggggaaa	ctgagctcag	agagagaaa	aacttgctca	aggtcaggaa
5641	gccagggtctc	ctgatgtctca	gtccgggttat	aacaccctgc	tttatttttct	tccattcaat
5701	aggaagttac	tgtgacccca	gacaagacct	agtcttggct	gtgggacaca	tgttttcttt
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5821	ctaatttttg	tagtttttagt	agagactggg	cttcaccatg	ttggccaggc	tggtttcgaa
5881	ctcctgacct	caggtgaccc	tcctgctcg	gcctcccaa	gtgctgaatt	acaggcgtga
5941	gccaccatgc	ccagctggga	cacatgtttt	ctgggagtca	agatgaggag	ttagggttca
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6121	gtcccacagg	tggaattcaa	gaagtcagga	agaggaaactt	ccttggggca	acactgaaga
6181	ggaactcccc	tggtgtgata	tcttattttt	ttaattatta	ttattttttt	gagatggagt
6241	ctcactctgt	ccctcaggct	ggagtacagt	ggcacaatct	tggctcactg	caacctccac
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[0256] Modifications may be made to the foregoing without departing from the basic aspects of the invention. Although the invention has been described in substantial detail with reference to one or more specific embodiments, those of skill in the art will recognize that changes may be made to the embodiments specifically disclosed in this application, yet these modifications and improvements are within the scope and spirit of the invention, as set forth in the aspects which follow. All publications or patent documents cited in this specification are incorporated herein by reference as if each such publication or document was specifically and individually indicated to be incorporated herein by reference.

[0257] Citation of the above publications or documents is not intended as an admission that any of the foregoing is pertinent prior art, nor does it constitute any admission as to the contents or date of these publications or documents. U.S. patents and other publications referenced herein are hereby incorporated by reference.

What is claimed is:

1. A method for identifying a subject at risk of osteoarthritis, which comprises detecting the presence or absence of one or more polymorphic variations associated with osteoarthritis in a nucleic acid sample from a subject, wherein the one or more polymorphic variations are detected in a nucleotide sequence selected from the group consisting of:

- (a) a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
- (b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
- (c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
- (d) a fragment of a nucleotide sequence of (a), (b), or (c);

whereby the presence of the polymorphic variation is indicative of the subject being at risk of osteoarthritis.

2. The method of claim 1, which further comprises obtaining the nucleic acid sample from the subject.

3. The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 31118000 to 31129000 in human genomic DNA.

4. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 1 selected from the group consisting of 247, 1535, 2386, 6440, 9133, 9143, 9471, 13150, 13717, 14466, 15769, 16870, 18545, 18749, 19123, 20736, 21038, 21046, 21050, 21056, 21706, 23170, 25028, 27871, 28070, 31717, 32019, 32318, 33080, 33101, 34236, 34285, 34818, 35168, 37981, 38113, 38117, 38481, 38615, 38944, 39288, 41385, 42136, 42185, 42353, 42434, 44580, 44675, 45739, 46439, 47457, 47735, 50319, 50708, 51185, 53002, 53064, 53637, 55274, 55825, 55986, 56684, 57653, 57659, 57692, 57775, 61313, 61431, 61699, 62906, 63619, 64664, 68452, 69665, 69681, 70091, 74637, 74760, 76523, 78559, 79549, 79882, 81339, 81681, 81696, 83517, 85431, 86332, 87358, 87725, 89052, 90020, 90231, 90284, 90447, 90601, 90724, 92559, 95176, 95195 and 96822.

5. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 1 selected from the group consisting of 13150, 21046, 23170, 25028, 44580, 62906, 64664 and 83517.

6. The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 36914000 to 36931000 in human genomic DNA.

7. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 2 selected from the group consisting of 211, 7217, 7895, 13308, 14279, 17026, 18271, 20417, 21843, 22069, 22145, 22519, 22539, 23236, 23256, 23402, 23499, 23620, 23871, 24136, 25427, 25866, 26541, 26576, 26689, 26720, 27113, 27164, 27186, 28341, 29160, 29844, 30665, 30830, 31061, 31523, 32326, 32346, 32358, 34909, 34975, 35066, 35096, 35375, 36304, 36712, 36770, 37342, 37412, 37884, 38077, 38300, 38301, 41189, 44408, 44493, 44571, 44670, 45219, 45258, 47261, 48473, 48771, 55292, 56479, 56747, 60620, 60688, 61058, 61129, 61577, 61961, 63351, 63926, 65798, 66043, 66044, 66246, 66318, 66547, 71238, 71283, 71492, 72274, 73762, 74209, 75284, 77347, 77589, 78096, 78606, 78862, 79135, 79146, 79456, 79609, 80086, 80119, 80766, 81110, 81269, 81668, 82433, 82559, 83298, 83821, 84121, 84147, 84543, 84554, 84691, 84727, 85678, 86699, 86700, 86792, 86832, 87045, 87140, 87365, 88342, 88498, 88589, 95502, 96968, 97448, 97568 and 98724.

8. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 2 selected from the group consisting of 23236, 32358, 47261, 48771, 55292, 60688, 72274, 74209, 77589, 79135, 79456, 79609, 80119, 80766, 81110, 82433, 84121, 84147, 85678, 86699, 86832, 87140 and 88589.

9. The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 76196500 to 76221500 in human genomic DNA.

10. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 3 selected from the group consisting of 218, 1440, 1442, 2611, 4317, 4724, 4788, 5202, 5780, 5974, 6644, 7430, 7938, 8095, 8183, 8312, 8352, 9348, 9378, 9617, 9727, 9834, 9899, 10211, 10377, 10695, 10729, 10730, 11433, 11951, 12697, 12982, 14419, 14501, 14983, 15280, 15475, 15888, 15976, 16307, 16442, 17255, 18948, 19435, 19753, 20021, 20022, 20503, 20590, 21804, 21919, 21990, 22412, 22536, 23432, 23468, 23772, 24325, 24773, 26274, 27440, 28561, 30071, 31764, 33008, 35310, 35460, 37112, 37285, 37747, 38057, 38859, 38860, 39525, 40216, 40281, 41453, 42091, 42513, 42935, 42985, 43003, 43281, 43716, 43866, 44234, 44596, 44871, 45005, 45282, 47178, 47816, 47887, 48134, 48135, 48276, 48400, 48798, 48803, 49146, 49969, 51059, 51064, 53285, 54560, 54748, 54785, 55102, 55644, 55705, 55841, 56623, 56825, 56827, 56892, 59150, 59958, 60231, 60524, 61871, 62226, 63230, 63468, 63787, 65732, 65989, 68832, 69904, 70365, 70886, 73088, 73103, 75934, 75966, 76273, 77943, 78466, 78861, 78872, 79836, 80908, 81509, 83576, 83662, 83782, 84282, 84444, 85129,

85151, 85296, 85809, 86387, 86494, 89786, 89894, 90122, 92067, 92187, 92312, 92824, 93733, 96553 and 96941.

11. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 3 selected from the group consisting of 4788, 8312, 9378, 9727, 9899, 10211, 27440, 40216, 40281, 42091, 43866, 48803, 51059, 55644, 56623, 73103, 78872, 79836, 85129, 92824 and 96941.

12. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in Table A.

13. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in linkage disequilibrium with one or more positions in claim 4, 7, 10 or 12.

14. The method of claim 1, wherein detecting the presence or absence of the one or more polymorphic variations comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to a nucleotide sequence in the nucleic acid and hybridizes to a region adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of a polymorphic variation in the extension products.

15. The method of claim 1, wherein the subject is a human.

16. The method of claim 15, wherein the subject is a human female.

17. The method of claim 15, wherein the subject is a human male.

18. A method for identifying a polymorphic variation associated with osteoarthritis proximal to an incident polymorphic variation associated with osteoarthritis, which comprises:

identifying a polymorphic variation proximal to the incident polymorphic variation associated with osteoarthritis, wherein the polymorphic variation is detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising a polymorphic variation;

determining the presence or absence of an association of the proximal polymorphic variant with osteoarthritis.

19. The method of claim 18, wherein the incident polymorphic variation is at one or more positions in claim 4, 7, 10 or 12.

20. The method of claim 18, wherein the proximal polymorphic variation is within a region between about 5 kb 5' of the incident polymorphic variation and about 5 kb 3' of the incident polymorphic variation.

21. The method of claim 18, which further comprises determining whether the proximal polymorphic variation is in linkage disequilibrium with the incident polymorphic variation.

22. The method of claim 18, which further comprises identifying a second polymorphic variation proximal to the identified proximal polymorphic variation associated with osteoarthritis and determining if the second proximal polymorphic variation is associated with osteoarthritis.

23. The method of claim 22, wherein the second proximal polymorphic variant is within a region between about 5 kb 5' of the incident polymorphic variation and about 5 kb 3' of the proximal polymorphic variation associated with osteoarthritis.

24. An isolated nucleic acid comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising a polymorphic variation; and

(e) a nucleotide sequence complementary to the nucleotide sequences of (a), (b), (c), or (d);

wherein the nucleotide sequence comprises a polymorphic variation associated with osteoarthritis selected from the group consisting of in SEQ ID NO: 1 a guanine at position 13150, a thymine at position 21046, an adenine at position 23170, an adenine at position 25028, a guanine at position 44580, a guanine at position 62906, a cytosine at position 64664 and a cytosine at position 83517; in SEQ ID NO: 2 an adenine at position 23236, a cytosine at position 32358, a guanine at position 47261, a guanine at position 48771, a cytosine at position 55292, an adenine at position 60688, a guanine at position 72274, a guanine at position 74209, a cytosine at position 77589, an adenine at position 79135, a thymine at position 79456, an adenine at position 79609, an adenine at position 80119, a cytosine at position 80766, an adenine at position 81110, a cytosine at position 82433, a cytosine at position 84121, a thymine at position 84147, a cytosine at position 85678, a thymine at position 86699, an adenine at position 86832, a guanine at position 87140 and an adenine at position 88589; in SEQ ID NO: 3 a guanine at position 4788, a thymine at position 8312, a deletion at position 9378, a cytosine at position 9727, a guanine at position 9899, a cytosine at position 10211, a guanine at position 27440, a guanine at position 40216, a cytosine at position 40281, an adenine at position 42091, a guanine at position 43866, an adenine at position 48803, an adenine at position 51059, an adenine at position 55644, a cytosine at position 56623, a cytosine at position 73103, an adenine at position 78872, a guanine at position 79836, a cytosine at position 85129, a guanine at position 92824 and an adenine at position 96941; and an allele associated with osteoporosis in Table A for positions rs552, rs12904, rs2282146, rs734784, rs1042164, rs749670, rs955592, rs1143016, rs755248, rs1055055, rs835409, rs927663, rs8162, rs831038, rs33079, rs1710880, rs4472029, rs799570, rs1282730, rs1518875, rs1568694, rs905042, rs1957723, rs794018, rs707723, rs893861, rs1914903, rs2062232, rs26609, rs1370987, rs1012414, rs435903, rs1248, rs703508, rs226465, rs241448, rs763155, rs1040461, rs462832, rs804194, rs1022646, rs1569112, rs805623, rs1019850, rs1599931, AA, rs279941, rs1062230, rs1859911, rs1477261, rs1191119, rs657780, rs1393890, rs1478714, rs868213, rs690115, rs1465501, rs899173, rs10477, rs926393, rs465271, rs13847 and rs738658.

25. An oligonucleotide comprising a nucleotide sequence complementary to a portion of the nucleotide sequence of (a), (b), (c), or (d) in claim 24, wherein the 3' end of the oligonucleotide is adjacent to a polymorphic variation associated with osteoarthritis.

26. A microarray comprising an isolated nucleic acid of claim 24 linked to a solid support.

27. An isolated polypeptide encoded by the isolated nucleic acid sequence of claim 24.

28. A method for identifying a candidate therapeutic for treating osteoarthritis, which comprises:

(a) introducing a test molecule to a system which comprises a nucleic acid comprising a nucleotide sequence selected from the group consisting of:

- (i) a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
- (ii) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
- (iii) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
- (iv) a fragment of a nucleotide sequence of (a), (b), or (c); or

introducing a test molecule to a system which comprises a protein encoded by a nucleotide sequence of (i), (ii), (iii), or (iv); and

(b) determining the presence or absence of an interaction between the test molecule and the nucleic acid or protein,

whereby the presence of an interaction between the test molecule and the nucleic acid or protein identifies the test molecule as a candidate therapeutic for treating osteoarthritis.

29. The method of claim 28, wherein the system is an animal.

30. The method of claim 28, wherein the system is a cell.

31. The method of claim 28, wherein the nucleotide sequence comprises one or more polymorphic variations associated with osteoarthritis.

32. The method of claim 31, wherein the one or more polymorphic variations associated with osteoarthritis are at one or more positions in claim 4, 7, 10 or 12.

33. A method for treating osteoarthritis in a subject, which comprises contacting one or more cells of a subject in need thereof with a nucleic acid, wherein the nucleic acid comprises a nucleotide sequence selected from the group consisting of:

- (a) a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
- (b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
- (c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;

(d) a fragment of a nucleotide sequence of (a), (b), or (c); and
(e) a nucleotide sequence complementary to the nucleotide sequences of (a), (b), (c), or (d);
whereby contacting the one or more cells of the subject with the nucleic acid treats the
osteoarthritis in the subject.

34. The method of claim 33, wherein the nucleic acid is RNA or PNA.

35. The method of claim 34, wherein the nucleic acid is duplex RNA.

36. A method for treating osteoarthritis in a subject, which comprises contacting one or more
cells of a subject in need thereof with a protein, wherein the protein is encoded by a nucleotide sequence
which comprises a polynucleotide sequence selected from the group consisting of:

- (a) a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
 - (b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in
SEQ ID NO: 1-3 or referenced in Table A;
 - (c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the
amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
 - (d) a fragment of a nucleotide sequence of (a), (b), or (c);
- whereby contacting the one or more cells of the subject with the protein treats the osteoarthritis
in the subject.

37. A method for treating osteoarthritis in a subject, which comprises:
detecting the presence or absence of one or more polymorphic variations associated with
osteoarthritis in a nucleic acid sample from a subject, wherein the one or more polymorphic variation are
detected in a nucleotide sequence selected from the group consisting of:

- (a) a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
- (b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in
SEQ ID NO: 1-3 or referenced in Table A;
- (c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the
amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
- (d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising a polymorphic
variation; and

administering an osteoarthritis treatment to a subject in need thereof based upon the presence or
absence of the one or more polymorphic variations in the nucleic acid sample.

38. The method of claim 37, wherein the one or more polymorphic variations are detected at one or more positions in claim 4, 7, 10 or 12.

39. The method of claim 37, wherein the treatment is selected from the group consisting of administering a corticosteroid, a nonsteroidal anti-inflammatory drug (NSAID), a cyclooxygenase-2 (COX-2) inhibitor, an antibody, a glucocorticoid, hyaluronic acid, chondrotin sulfate, glucosamine or acetaminophen; prescribing a heat/cold regimen or a joint protection regimen; performing joint surgery; prescribing a weight control regimen; and combinations of the foregoing.

40. A method for detecting or preventing osteoarthritis in a subject, which comprises:
detecting the presence or absence of one or more polymorphic variations associated with osteoarthritis in a nucleic acid sample from a subject, wherein the polymorphic variation is detected in a nucleotide sequence selected from the group consisting of:
(a) a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising a polymorphic variation; and
administering an osteoarthritis prevention or detection procedure to a subject in need thereof based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample.

41. The method of claim 40, wherein the one or more polymorphic variations are detected at one or more positions in claim 4, 7, 10 or 12.

42. The method of claim 40, wherein the osteoarthritis prevention is selected from the group consisting of administering a corticosteroid, a nonsteroidal anti-inflammatory drug (NSAID), a cyclooxygenase-2 (COX-2) inhibitor, an antibody, a glucocorticoid, hyaluronic acid, chondrotin sulfate, glucosamine or acetaminophen; prescribing a heat/cold regimen or a joint protection regimen; performing joint surgery; prescribing a weight control regimen; and combinations of the foregoing.

43. A method of targeting information for preventing or treating osteoarthritis to a subject in need thereof, which comprises:

detecting the presence or absence of one or more polymorphic variations associated with osteoarthritis in a nucleic acid sample from a subject, wherein the polymorphic variation is detected in a nucleotide sequence selected from the group consisting of:

- (a) a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
- (b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
- (c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A;
- (d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising a polymorphic variation; and

directing information for preventing or treating osteoarthritis to a subject in need thereof based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample.

44. The method of claim 43, wherein the one or more polymorphic variations are detected at one or more positions in claim 4, 7, 10 or 12.

45. A composition comprising a cell from a subject having osteoarthritis or at risk of osteoarthritis and an antibody that specifically binds to a protein, polypeptide or peptide encoded by a nucleotide sequence identical to or 90% or more identical to a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A.

46. The composition of claim 45, wherein the antibody specifically binds to an epitope comprising an amino acid encoded by rs734784, rs1042164, rs749670, rs955592 and rs1040461.

47. A composition comprising a cell from a subject having osteoarthritis or at risk of osteoarthritis and a RNA, DNA, PNA or ribozyme molecule comprising a nucleotide sequence identical to or 90% or more identical to a portion of a nucleotide sequence in SEQ ID NO: 1-3 or referenced in Table A.

48. The composition of claim 47, wherein the RNA molecule is a short inhibitory RNA molecule.

Abstract of the Disclosure

Provided herein are methods for identifying a risk of osteoarthritis in a subject, reagents and kits for carrying out the methods, methods for identifying candidate therapeutics for treating osteoarthritis, and therapeutic and preventative methods applicable to osteoarthritis. These embodiments are based upon an analysis of polymorphic variations in nucleotide sequences within the human genome.

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FIGURE 1A

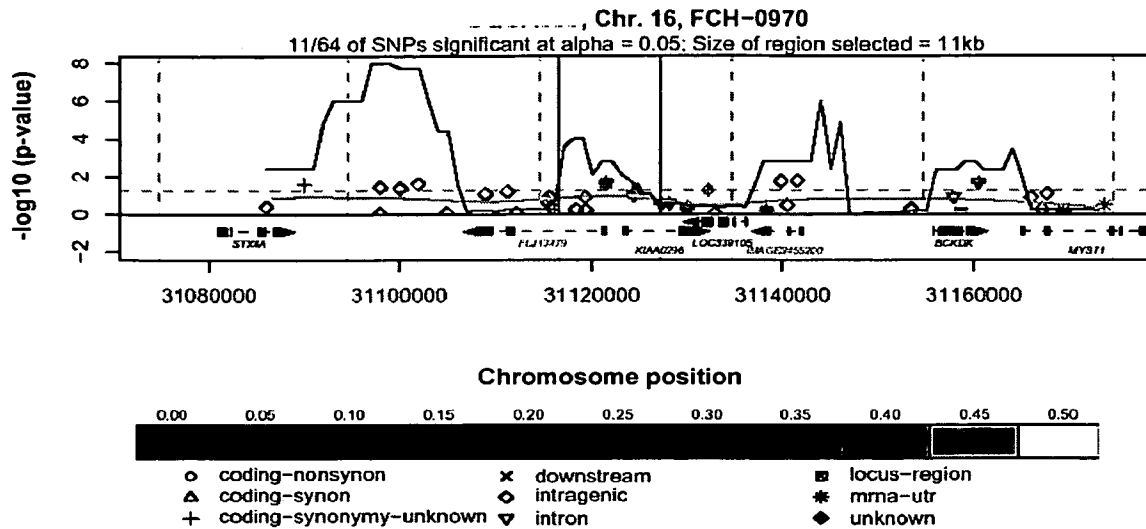
KIAA0296 – DISCOVERY P-VALUES (female only)

FIGURE 1B

CHROM 4 – DISCOVERY P-VALUES (female only)

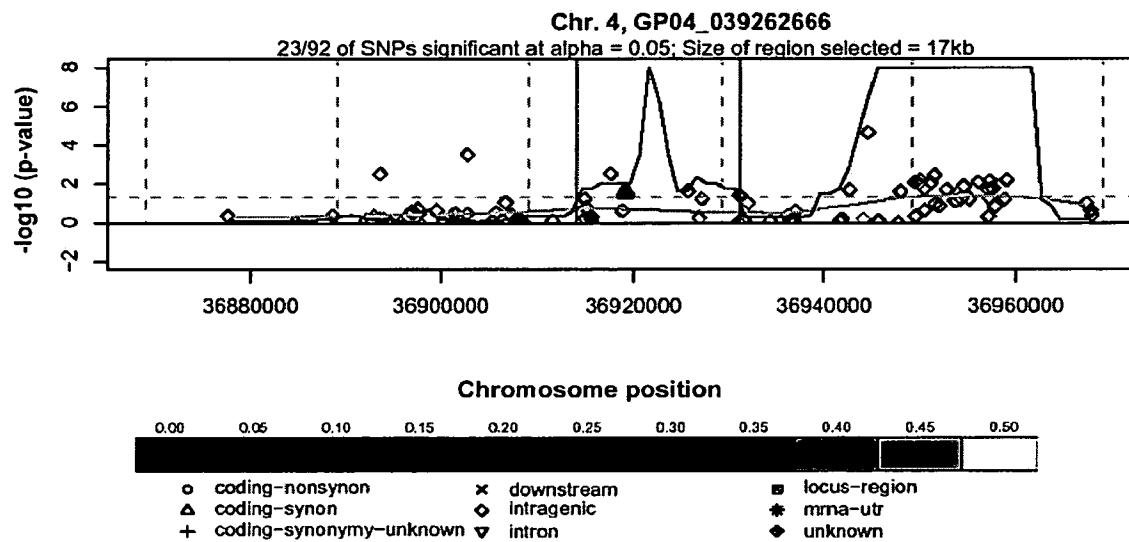
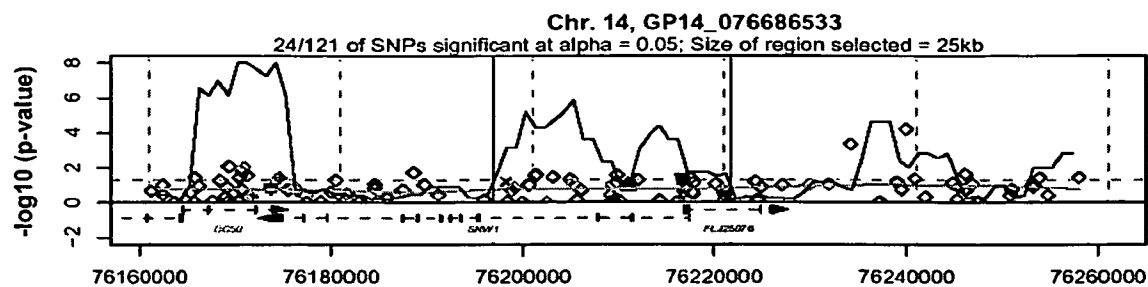
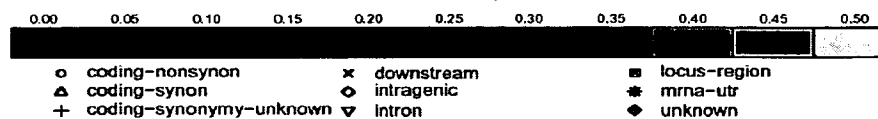


FIGURE 1C

SNW1 – DISCOVERY P-VALUES (female only)



Chromosome position



Application Data Sheet

Application Information

Application Type::	Provisional
Subject Matter::	Utility
Suggested Group Art Unit::	Not Yet Assigned
CD-ROM or CD-R?::	None
Sequence submission?::	None
Computer Readable Form (CRF)?::	No
Title::	METHODS FOR IDENTIFYING RISK OF OSTEOARTHRITIS AND TREATMENTS THEREOF
Attorney Docket Number::	524593008600
Request for Early Publication?::	No
Request for Non-Publication?::	No
Total Drawing Sheets::	2
Small Entity?::	Yes
Petition included?::	No
Secrecy Order in Parent Appl.?::	No

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